SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Screening of genes to give tolerance against
   environmental stress and the apprications

<130> YG12-12PCT

<140>
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<150> JP P1999-235910
<151> 1999-07-19

<150> JP P2000-85377
<151> 2000-03-24

<160> 72

<170> PatentIn Ver. 2.1

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<213> Bruguiera sexangula

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Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys Val Val Gly Pro Ala
                 10              15                  20


aga tca aag agt gct act gta ccc acc caa aca gta ttg cct ttc aag    152
Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys
                 25              30                  35


ttc aca aac ccg tcg tta ctc act cga tcg cta agc ttt tca tca aaa    200
Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys
                 40              45                  50


ggt tca agc ttt gac agc ttc tct gta ccc aaa aga tct ttt tct tgc    248
Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys Arg Ser Phe Ser Cys
                 55              60                  65


aga agc caa gcc act cca tct gat gat gcc tca aga ccc acc aaa gtt    296
Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser Arg Pro Thr Lys Val
70                   75              80                  85


caa gag ctg tgt gtg tat gag atg aac gag aga gat cgt gga agc cct    344
Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg Asp Arg Gly Ser Pro
                 90              95                  100


gct gtt ctc cgg ttg agc cag aaa cct gtt aat tct ctc ggc gat ctc    392
Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn Ser Leu Gly Asp Leu
                 105             110                 115


gtg cct ttc agt aac aaa gtt tac agc gga gac ctg cag aag cga att    440
Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp Leu Gln Lys Arg Ile
                 120             125                 130


gga gta acc gca gaa tat gca tcc tgatccaaaa caagccagaa aaaaagggtg    494
Gly Val Thr Ala Glu Tyr Ala Ser
                 135             140
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atcgctttga agcgatatat agcttttatt tcggtggcta tggtcacatt gctgtgcaag 554

gcgcatactt gacctacgag gacacgcacc ttgctgtgac gggcgggtcg ggcatatttg 614

aaggagtgtc tggtcaggtt aagctgcagc aactcgtgta ccctttcaag ctcttctaca 674

ctttctactt gcgaggcatc aaggacttgc cggaggagct tacgaagaag ccggttgagc 734

cccacccttc tgttgagccg atgccggcgg ccaaggcttg cgagccacat gccgttgttg 794

ctaatttcac cgattagtga ttaattgtcc ttttgggggtt cggatgaact tgagttagct 854

tacagttgca caacgttatg gcgcgagaca cgagagggaa ccttagccat aagaaaatta 914

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<213> Bruguiera sexangula

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Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr
                20                  25                  30

Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu
        35                  40                  45

Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys
    50                  55                  60

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Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
65                  70                  75                  80


Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
                85                  90                  95


Asp Arg Gly Ser Pro Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn
            100                 105                 110


Ser Leu Gly Asp Leu Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp
        115                 120                 125


Leu Gln Lys Arg Ile Gly Val Thr Ala Glu Tyr Ala Ser
    130                 135                 140
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<213> Bruguiera sexangula

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                      Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu
                       1               5                  10
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ggc gaa cgt cag tcc ggc cag gac gtc cgc act caa aat gtg gtg gca   161
Gly Glu Arg Gln Ser Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala
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tgt caa gcg gtt gcc aat att gtc aaa tct tca ctt ggt cct gtc gga      209
Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly
         30                    35                    40

ctc gac aag atg cta gtg gat gat att ggt gat gta aca att aca aat      257
Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn
         45                    50                    55

gat ggt gct acg att ctt aag atg tta gaa gta gag cat cct gca gca      305
Asp Gly Ala Thr Ile Leu Lys Met Leu Glu Val Glu His Pro Ala Ala
60                    65                    70                    75

aag gtg ctc gtg gag ttg gct gag ctt caa gac cga gaa gtt gga gat      353
Lys Val Leu Val Glu Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp
                   80                    85                    90

gga acc act tcg gtt gtc atc ata gca gct gag ttg ctc aag aga gca      401
Gly Thr Thr Ser Val Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala
                   95                   100                   105

aat gat ctc gtg agg aat aag atc cac cca aca tca ata atc agt gga      449
Asn Asp Leu Val Arg Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly
         110                   115                   120

tac agg ctt gct atg agg gaa gca tgc aag tat gtt gaa gag aaa ttg      497
Tyr Arg Leu Ala Met Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu
         125                   130                   135

tca atg aag gtt gaa aag ctt gga aaa gat tct cta gta aac tgt gca      545
Ser Met Lys Val Glu Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala
140                   145                   150                   155

aag aca agc atg tcc tca aag ttg ata gct ggt gac agc gac ttc ttt      593
Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe

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                    160                 165                 170

gca aat ttg gtt gta gat gct gta caa gca gta aag atg acc aat gca    641
Ala Asn Leu Val Val Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala
            175                 180                 185


cgg ggg gaa atc aaa tat cct atc aag agt ata aat att ttg aaa gct    689
Arg Gly Glu Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala
        190                 195                 200


cat gga aaa agt gca aga gat agc tgc ctt ttg aat ggc tat gct ctc    737
His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu
        205                 210                 215


aat act ggt cgt gct gct caa ggg atg cct atg aga gtt gca cct gca    785
Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala
220                 225                 230                 235


agg att gct tgt ctt gac ttt aat ctt cag aaa acg aag atg caa ttg    833
Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu
                240                 245                 250


ggt gta caa gtc tta gtc act gat ccc agg gag ctt gaa aga att cgt    881
Gly Val Gln Val Leu Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg
            255                 260                 265


caa aga gaa gct gat atg aca aag gaa cgg att gag aaa ctc ctg aaa    929
Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys
            270                 275                 280


gct gga gca aat gtt gtt cta acc aca aag gga att gat gac atg gca    977
Ala Gly Ala Asn Val Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala
        285                 290                 295


ctt aaa tat ttt gtg gag gct ggg gct att gct gtg aga cgt gtt cgg    1025
Leu Lys Tyr Phe Val Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg
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aaa gag gat atg cgc cat gtt gcc aag gca act ggt gca aca ctg gtt     1073
Lys Glu Asp Met Arg His Val Ala Lys Ala Thr Gly Ala Thr Leu Val
                    320                     325                     330


tca aca ttt gct gac atg gaa gga gag gaa aca ttt gat tca tca ctg     1121
Ser Thr Phe Ala·Asp Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu
                    335                     340                     345


ctt gga caa gct gaa gaa gtt gtg gag gag cgc att gct gat gac gat     1169
Leu Gly Gln Ala Glu Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp
              350                     355                     360


gtg att atg ata aaa ggg aca aag act aca agt gcg gtt tcc ttg att     1217
Val Ile Met Ile Lys Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile
        365                     370                     375


ctt cgt ggt gca aat gac tat atg ctc gat gag atg gag cga gcc ctg     1265
Leu Arg Gly Ala Asn Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu
380                     385                     390                     395


cat gat gct tta tgt att gtc aag aga acc ctt gaa tct aat aca gta     1313
His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val
                    400                     405                     410


gtt gca ggt gga ggt gct gtt gag gct gcc ttg tct gtg cac ttg gag     1361
Val Ala Gly Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu
              415                     420                     425


tac ctc gct aca act ctt ggg tca cga gag cag tta gca ata gca gag     1409
Tyr Leu Ala Thr Thr Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu
              430                     435                     440


ttt gca gaa tcc ttg ttg att ata cca aag gtt ctt gct gtc aat gct     1457
Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala

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gcc aaa gat gcc act gaa tta gct gca aaa ctc cgg gct tac cac cat    1505
Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His
460              465              470              475


aca gca caa aca aag gct gat aag aaa cat tta tca agc atg gga cta    1553
Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu
                 480              485              490


gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att    1601
Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile
                 495              500              505


gaa cct gca atg agc aaa ata aag ata att cag ttt gct act gaa gca    1649
Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala
         510              515              520


gcc ata aca att ctt cga att gat gac atg atc aag ctt gtc aag gat    1697
Ala Ile Thr Ile Leu Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp
         525              530              535


gag act cag aat gaa gag gaa tagatgcaga ctcttgtaag ctgcctccct        1748
Glu Thr Gln Asn Glu Glu Glu
540              545


tttgttttca aatttgtgtc ccttgcgagc tggaggaaag ggggggtgtt tatgtggtgt  1808

tttcagtggt tttaattttt caaggagctc gcggcctgtg tactttaggt tagagtccat  1868

ccaaggggtg tttattggat aatgcctaag ctgtttctcg tctattagta ggctggtagt  1928

tccactgagt tctcatccca attaaaagaa tgagatcaaa gggtcctaaa ttcgtactca  1988

ttggtgcacg atttgtttct gacaagcata agacttgacc ctctctatca caataaaaaa  2048
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<211> 546

<212> PRT

<213> Bruguiera sexangula

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Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu Gly Glu Arg Gln Ser
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Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala Cys Gln Ala Val Ala
            20              25              30

Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly Leu Asp Lys Met Leu
            35              40              45

Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile
            50              55              60

Leu Lys Met Leu Glu Val Glu His Pro Ala Ala Lys Val Leu Val Glu
65              70              75              80

Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp Gly Thr Thr Ser Val
                85              90              95

Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala Asn Asp Leu Val Arg
            100             105             110

Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly Tyr Arg Leu Ala Met
            115             120             125

Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu Ser Met Lys Val Glu
            130             135             140

Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala Lys Thr Ser Met Ser
145                 150                 155                 160

Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe Ala Asn Leu Val Val
                165                 170                 175

Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala Arg Gly Glu Ile Lys
                180                 185                 190

Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala His Gly Lys Ser Ala
                195                 200                 205

Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala
                210                 215                 220

Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala Arg Ile Ala Cys Leu
225                 230                 235                 240

Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu Gly Val Gln Val Leu
                245                 250                 255

Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg Gln Arg Glu Ala Asp
                260                 265                 270

Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys Ala Gly Ala Asn Val
                275                 280                 285

Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala Leu Lys Tyr Phe Val
                290                 295                 300

Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg Lys Glu Asp Met Arg
305                 310                 315                 320

His Val Ala Lys Ala Thr Gly Ala Thr Leu Val Ser Thr Phe Ala Asp
                325                 330                 335

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Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu Leu Gly Gln Ala Glu
        340             345             350

Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp Val Ile Met Ile Lys
        355             360             365

Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile Leu Arg Gly Ala Asn
    370             375             380

Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu His Asp Ala Leu Cys
385             390             395             400

Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val Val Ala Gly Gly Gly
            405             410             415

Ala Val Glu Ala Ala Leu Ser Val His Leu Glu Tyr Leu Ala Thr Thr
        420             425             430

Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu Phe Ala Glu Ser Leu
        435             440             445

Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala Ala Lys Asp Ala Thr
    450             455             460

Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His Thr Ala Gln Thr Lys
465             470             475             480

Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu Asp Leu Ser Lys Gly
        485             490             495

Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile Glu Pro Ala Met Ser
        500             505             510

Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala Ala Ile Thr Ile Leu
    515             520             525
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Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp Glu Thr Gln Asn Glu
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Glu Glu
545



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<212> DNA
<213> Bruguiera sexangula

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                             Met Ser Cys Cys Gly Gly Asn Cys Gly
                              1               5

tgc gga gca agc tgc aat tgc ggc aac ggc tgt gga ggg tgc aag atg   100
Cys Gly Ala Ser Cys Asn Cys Gly Asn Gly Cys Gly Gly Cys Lys Met
 10              15                  20                  25

tac cca gac atg ggc ttc gcc gag aag acc act acc gag act ctg gtt   148
Tyr Pro Asp Met Gly Phe Ala Glu Lys Thr Thr Thr Glu Thr Leu Val
             30                  35                  40

ctc ggc gtg ggg cct gag agg gcc cac ttt gag gga gcc gag atg ggc   196
Leu Gly Val Gly Pro Glu Arg Ala His Phe Glu Gly Ala Glu Met Gly
             45                  50                  55

gtg ccg gcc gag aac gga ggc tgc aag tgc gga agt aac tgc acc tgc   244
Val Pro Ala Glu Asn Gly Gly Cys Lys Cys Gly Ser Asn Cys Thr Cys

gac ccc tgc act tgt aaa tgaggggaaa gtgacaggga aggtccgatc            292
Asp Pro Cys Thr Cys Lys
        75

tattattagt ctatatgtgt gtgttgggag tcttgcttac aataaaccag tcatgccttg 352

cgtttcctcc atgcgcagat cttaggtttt aggatatctc tgtggtttct ccaagctatg 412

gattttcagt gtctagtttt cctgtattac aaggatagtt tataaccgta tatgcatggt 472

cggaatcctt ccaaccattt cgtttgtcta aatatatata tgtgtgtgtg tgtgtgtgtt 532

tgatgggaaa gtgagcttct ttatgtttta tgactaaaaa aaaaaaaaaa aaaaaa      588


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 1               5                  10                  15

Gly Asn Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Gly Phe Ala
            20                  25                  30

Glu Lys Thr Thr Thr Glu Thr Leu Val Leu Gly Val Gly Pro Glu Arg
        35                  40                  45

Ala His Phe Glu Gly Ala Glu Met Gly Val Pro Ala Glu Asn Gly Gly
    50                  55                  60

Cys Lys Cys Gly Ser Asn Cys Thr Cys Asp Pro Cys Thr Cys Lys

<210> 7
<211> 1280
<212> DNA
<213> Bruguiera sexangula

<220>
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<222> (1)..(1002)

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Ile Glu Gly Glu Val Val Glu Val Gln Ile Asp Arg Pro Ala Val Thr
 1               5                   10                  15


ggc gcc gcg tcc aag acg ggg aaa ttg acg cta aag acg acg gag atg    96
Gly Ala Ala Ser Lys Thr Gly Lys Leu Thr Leu Lys Thr Thr Glu Met
            20                  25                  30


gag acg gtg tac gat ttg ggg gcg aaa atg ata gag gca ttg ggg aag    144
Glu Thr Val Tyr Asp Leu Gly Ala Lys Met Ile Glu Ala Leu Gly Lys
            35                  40                  45


gaa aag gtg cag agt ggg gat gtt att gca att gac aag gcg tcc ggc    192
Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly
        50                  55                  60


aaa att aca aag ctt ggg cgt tca ttt tcg cgg tct agg gat tac gat    240
Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp
65                  70                  75                  80


gcc atg gga cca cag gtg aag ttt gtt cag tgc cct gat ggg gag ctg    288
Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu

cag aag agg aaa gag gtc gtg cat tgt gtc tca ctg cac gag att gat    336
Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp
            100               105               110

gtt atc aat agc aga aca cag ggg ttt ctt gct ctt ttc acc ggg gat    384
Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp
            115               120               125

act ggt gaa atc cgt gcg gag gtg agg gaa caa att gac aca aag gtg    432
Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val
        130               135               140

gct gaa tgg aga gag gaa ggg aaa gca gag att gtg cca ggt gtc ctc    480
Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu
145               150               155               160

ttt att gat gag gtc cac atg ctt gac att gag tgc ttc tca ttt ctg    528
Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu
                165               170               175

aat cgt gct ctt gag aat gag atg gcg cca ata tta gtt gtt gct acc    576
Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr
            180               185               190

aac aga ggg atc acc aca atc aga ggc aca aat tac aaa tct cct cat    624
Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His
            195               200               205

ggg att cca ata gat ctc ctt gat cga cta ctc att atc aca act caa    672
Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln
        210               215                 220

cct tac aca aag gat gaa att cgt aag att ctg gat atc aga tgt cag    720
Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln

gaa gaa gat gtg gag atg gct gaa gag gca aag gct ttg tta aca cat    768
Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His
                245                        250                        255

att ggg gca gaa aca tcc ttg aga tat gcc atc cat ctc att act gct    816
Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala
                260                        265                        270

gca gca ttg gca tgc cag aag cga aag gga aag ctt gtg gaa act gag    864
Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu
                275                        280                        285

gac att agt cga gct tac aat ctg ttt ctt gat gta aag aga tct aca    912
Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr
                290                        295                        300

cag tac cta ata gag tat cag aat cag tac atg ttt aat gag gca ccg    960
Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro
305                        310                        315                        320

gta gga gaa ggg gac gaa gaa ggg gcc aat gcc atg ctt tct    1002
Val Gly Glu Gly Asp Glu Glu Gly Ala Asn Ala Met Leu Ser
                325                        330

tgaagggcca taagctatgg agtctttgtg aaacccttct ccctacttta ttcgcagcac 1062

gagccctgaa atgaagaaca atggtagact tggatcccac cttggccctt atgtatgtct 1122

tctggaattg aaaaaagagt ccaagaaatt tgaatttcat gaaattggag aactgaactg 1182

tgcttactaa attgctactt tgcaagtaat gatagggcac tcacgcttga ctggctaagt 1242

atttatgttt ttatcatcaa aaaaaaaaaa aaaaaaa    1280

<210> 8
<211> 334
<212> PRT
<213> Bruguiera sexangula

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Ile Glu Gly Glu Val Val Glu Val Gln Ile Asp Arg Pro Ala Val Thr
1               5                   10                  15


Gly Ala Ala Ser Lys Thr Gly Lys Leu Thr Leu Lys Thr Thr Glu Met
                20                  25                  30


Glu Thr Val Tyr Asp Leu Gly Ala Lys Met Ile Glu Ala Leu Gly Lys
                35                  40                  45


Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly
        50                  55                  60


Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp
65                  70                  75                  80


Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu
                85                  90                  95


Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp
                100                 105                 110


Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp
                115                 120                 125


Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val
        130                 135                 140


Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu
145                 150                 155                 160

Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu
165                     170                     175

Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr
180                     185                     190

Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His
195                     200                     205

Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln
210                     215                     220

Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln
225                     230                     235                     240

Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His
245                     250                     255

Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala
260                     265                     270

Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu
275                     280                     285

Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr
290                     295                     300

Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro
305                     310                     315                     320

Val Gly Glu Gly Asp Glu Glu Gly Ala Asn Ala Met Leu Ser
325                     330

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<212> DNA
<213> Bruguiera sexangula

<220>
<221> CDS
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<400> 9
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                                 Met Gly His Ser Asn Val Trp Asn Ser
                                  1               5


cac ccc aag aac tac ggc cct ggt tcc cgc gcc tgt cgg gtg tgt ggg   101
His Pro Lys Asn Tyr Gly Pro Gly Ser Arg Ala Cys Arg Val Cys Gly
 10              15              20              25


aat ccg cac ggg ttg atc agg aag tac gga ctc atg tgc tgc aga cag   149
Asn Pro His Gly Leu Ile Arg Lys Tyr Gly Leu Met Cys Cys Arg Gln
             30              35              40


tgc ttc cgt agc aat gcc aag gaa att ggc ttc att aag tac cgc       194
Cys Phe Arg Ser Asn Ala Lys Glu Ile Gly Phe Ile Lys Tyr Arg
             45              50              55


tgaatgatat cgatatggcc cagaatggcc tgtggcggtg cgtgttcgat ttcagtagtt 254


cccctctttc ggatgagctt taggacaatg ttctctttag tttatgtatt gttgaacttg 314


gactgatgtt gaactaacga tattctggaa tcatttgata tttcgagagt ttattatttt 374


gatcatcatc ctcttgcttc tctgcttaaa aaaaaaaaaa aaaaaa              420


<210> 10

<210> 56

<211> 56

<212> PRT

<213> Bruguiera sexangula

<400> 10

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Met Gly His Ser Asn Val Trp Asn Ser His Pro Lys Asn Tyr Gly Pro
 1               5                   10                  15

Gly Ser Arg Ala Cys Arg Val Cys Gly Asn Pro His Gly Leu Ile Arg
            20                  25                  30

Lys Tyr Gly Leu Met Cys Cys Arg Gln Cys Phe Arg Ser Asn Ala Lys
            35                  40                  45

Glu Ile Gly Phe Ile Lys Tyr Arg
        50                  55
```

<210> 11

<211> 1664

<212> DNA

<213> Bruguiera sexangula

<220>

<221> CDS

<222> (34)..(1380)

<400> 11

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tctctcttta caggttaaag ctaagacttt ata atg ggt aag gag aag att cac   54
                                      Met Gly Lys Glu Lys Ile His
                                       1               5

att aac att gtg gtt att ggc cat gtc gac tcc gga aag tca acc aca   102
Ile Asn Ile Val Val Ile Gly His Val Asp Ser Gly Lys Ser Thr Thr
        10                  15                  20
```

```
act ggc cac ttg att tac aag ctt gga ggt atc gac aag cgt gtg att    150
Thr Gly His Leu Ile Tyr Lys Leu Gly Gly Ile Asp Lys Arg Val Ile
        25              30              35

gag agg ttt gag aag gaa gct gct gag atg aac aag agg tca ttc aag    198
Glu Arg Phe Glu Lys Glu Ala Ala Glu Met Asn Lys Arg Ser Phe Lys
    40              45              50              55

tat gcc tgg gtg ctt gac aag ctg aag gct gag cgt gag cgt ggt atc    246
Tyr Ala Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile
                60              65              70

acc att gat att gcc ttg tgg aag ttc gag aca acc aaa tat tac tgc    294
Thr Ile Asp Ile Ala Leu Trp Lys Phe Glu Thr Thr Lys Tyr Tyr Cys
            75              80              85

acg gtc att gat gct cct gga cat cgt gac ttt att aag aat atg atc    342
Thr Val Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile
        90              95              100

acc ggg act tcc caa gct gac tgt gct gtc ctc atc att gac tct acc    390
Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp Ser Thr
    105             110             115

act ggt ggc ttt gag gct ggt atc tct aaa gat ggt cag acc cgc gag    438
Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr Arg Glu
120             125             130             135

cat gcc ctg ctt gcc ttc acc ctt ggt gtt aag caa atg att tgc tgc    486
His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile Cys Cys
                140             145             150

tgc aac aag atg gat gct acc act tcc aag tat tct aag gca aga tat    534
Cys Asn Lys Met Asp Ala Thr Thr Ser Lys Tyr Ser Lys Ala Arg Tyr
            155             160             165
```

```
gat gaa att gtt aag gaa gtg tca tcc tac ttg aag aag gtt ggt tac    582
Asp Glu Ile Val Lys Glu Val Ser Ser Tyr Leu Lys Lys Val Gly Tyr
        170             175             180


aac cca gag aag att cct ttt gtc ccc ata tct gga ttt gag ggt gac    630
Asn Pro Glu Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu Gly Asp
        185             190             195


aac atg att gag aga tcc acc aac ctt gac tgg tac aag ggc cca act    678
Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly Pro Thr
200             205             210             215


ctt ctt gag gcc ctg gac atg atc cag gag cca aag agg cca tca gat    726
Leu Leu Glu Ala Leu Asp Met Ile Gln Glu Pro Lys Arg Pro Ser Asp
                220             225             230


aag ccc ctc cgt ctc cca ctt cag gat gtg tac aag att ggt ggt att    774
Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly Gly Ile
                235             240             245


ggg aca gtc cca gtg ggt cgt gtt gaa act ggt gtc ctg aag cct gga    822
Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu Lys Pro Gly
                250             255             260


atg gtt gtt act ttt ggt ccc tca gga ctg acc act gaa gtt aag tct    870
Met Val Val Thr Phe Gly Pro Ser Gly Leu Thr Thr Glu Val Lys Ser
        265             270             275


gtg gag atg cac cat gaa gct ctc caa gag gct ctt ccc gga gac aac    918
Val Glu Met His His Glu Ala Leu Gln Glu Ala Leu Pro Gly Asp Asn
280             285             290             295


gtt ggc ttc aat gtt aag aat gtt tcc gtg aag gat ctt aag cgg ggt    966
Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Leu Lys Arg Gly
                300             305             310
```

```
tat gtt gcc tca aac tcc aag gat gat cct gcc aag gag gca tct agc    1014
Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Glu Ala Ser Ser
                315             320             325


ttc acc tcc caa gtt atc atc atg aac cac cct ggt cag att gga aat    1062
Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile Gly Asn
                330             335             340


ggt tat gcc cct gtt ctg gat tgc cac acc tct cac att gct gtc aag    1110
Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala Val Lys
            345             350             355


ttt tct gag atc ctc aca aag att gat agg cga tct ggc aag gag ctt    1158
Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys Glu Leu
360             365             370             375


gaa aag gag ccc aag ttc ttg aag aat ggt gat gct ggg ttc gtg aag    1206
Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Phe Val Lys
                380             385             390


atg att ccg acc aag cct atg gtg gtg gaa act ttc tcc gag tat cct    1254
Met Ile Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu Tyr Pro
                395             400             405


ccg ctt ggt aga ttt gcc gtc agg gac atg cgc cag act gtt gca gtg    1302
Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val Ala Val
            410             415             420


gga gtc atc aag agt gtc gag aaa aag gaa cct tct gga gct aag gtg    1350
Gly Val Ile Lys Ser Val Glu Lys Lys Glu Pro Ser Gly Ala Lys Val
            425             430             435


act aaa tct gct gcc aag aag ggt ggc aaa tgaaccgtgc aagtcagagt    1400
Thr Lys Ser Ala Ala Lys Lys Gly Gly Lys
440             445
```

tgatgtagat gaaggctatt ggaagaataa agactgggcc ctggttagcg gtctaattat 1460

tggatgttca gcagttggtt tcgagaacta cagtttcaat tcagcgccat catcacggag 1520

ctgttgttcc cagaattggg ttcttgaccg tcggtggcat tggctgttgg tttgagtgac 1580

ttctttgtgt catgtttaga ctttatcgga tttgctattt cataaagcgg cttgggaatt 1640

ttaaaaaaaa aaaaaaaaaa aaaa                                        1664


<210> 12
<211> 449
<212> PRT
<213> Bruguiera sexangula

<400> 12
Met Gly Lys Glu Lys Ile His Ile Asn Ile Val Val Ile Gly His Val
 1               5                  10                  15


Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
            20                  25                  30


Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
            35                  40                  45


Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
        50                  55                  60


Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
65                  70                  75                  80


Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
                85                  90                  95

```
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
            100                 105                 110

Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
            115                 120                 125

Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly
            130                 135                 140

Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Ser
145                 150                 155                 160

Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Val Lys Glu Val Ser Ser
                165                 170                 175

Tyr Leu Lys Lys Val Gly Tyr Asn Pro Glu Lys Ile Pro Phe Val Pro
                180                 185                 190

Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu
                195                 200                 205

Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Met Ile Gln
            210                 215                 220

Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp
225                 230                 235                 240

Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu
                245                 250                 255

Thr Gly Val Leu Lys Pro Gly Met Val Val Thr Phe Gly Pro Ser Gly
                260                 265                 270

Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ala Leu Gln
                275                 280                 285
```

Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser
    290                 295                 300

Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp
305                 310                 315                 320

Pro Ala Lys Glu Ala Ser Ser Phe Thr Ser Gln Val Ile Ile Met Asn
                325                 330                 335

His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His
                340                 345                 350

Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp
            355                 360                 365

Arg Arg Ser Gly Lys Glu Leu Glu Lys Glu Pro Lys Phe Leu Lys Asn
    370                 375                 380

Gly Asp Ala Gly Phe Val Lys Met Ile Pro Thr Lys Pro Met Val Val
385                 390                 395                 400

Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
                405                 410                 415

Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Glu Lys Lys
                420                 425                 430

Glu Pro Ser Gly Ala Lys Val Thr Lys Ser Ala Ala Lys Lys Gly Gly
            435                 440                 445

Lys

<210> 13

<211> 770
<212> DNA
<213> Bruguiera sexangula

<220>
<221> CDS
<222> (2)..(769)

<400> 13
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c gat gat atg gac gag gcc aca ccc acc ttt gtt tgg ggc acc aat atc  49
  Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile
   1               5                  10                  15


agc gtg cag gat gtc aag gcc gct att cag atg ttt ttg aag cac ttc   97
Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe
             20                  25                  30


agg gat agt aat cag agt caa agg aac gag att ttt gaa gaa ggg aag  145
Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys
         35                  40                  45


tac gtg aaa gcg ata cat aag gtt ctt gaa gtt gaa gga gag tcg ctt  193
Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu
     50                  55                  60


gat gtt gat gct cgt gat gtg ttt gat tat gat tct gat ttg tat gcc  241
Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala
 65                  70                  75                  80


aag atg att cgg tac cca ctt gag gtt ttg gcc att ttc gac att gtt  289
Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val
                 85                  90                  95


ttg atg gat att gtg agt ttg atc aac cct ttg ttt gag aaa cat gta  337
Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val
            100                 105                 110
```

caa gtc agg att ttc aat ctt aag acc tcg att aca atg aga aat ctc   385
Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu
        115               120               125

aac cct tct gat atc gaa aag atg gtg tca ttg aag gga atg ata att   433
Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile
        130               135               140

cgg tgt agt tcc ata ata ccg gag atc agg gaa gca gta ttt aga tgc   481
Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys
145               150               155               160

ctt gtt tgt ggc tac ttc tct gat ccc atc gtt gtg gat aga gga cgg   529
Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg
                165               170               175

ata agt gaa cct aaa gca tgc ttg aaa gag gaa tgt ctt act aag aac   577
Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn
                180               185               190

tcc atg aca cta gtt cac aat cgt tgc agg ttt gct gat aag cag att   625
Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile
        195               200               205

gtg agg ctc cag gag aca cct gac gag atc cct gaa gga gga aca cca   673
Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro
        210               215               220

cac acg gtg agc tta ttg atg cat gac aag ctg gta gat gct gga aag   721
His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys
225               230               235               240

cca ggt gac agg gtt gag gtc act gga att tat agg gct atg agt gtt a 770
Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val
                245               250               255

<210> 14

<211> 256

<212> PRT

<213> Bruguiera sexangula

<400> 14

Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile
1               5                   10                  15

Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe
            20                  25                  30

Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys
            35                  40                  45

Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu
        50                  55                  60

Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala
65                  70                  75                  80

Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val
                85                  90                  95

Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val
                100                 105                 110

Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu
        115                 120                 125

Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile
        130                 135                 140

Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys

```
145                 150                 155                 160


Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg
                165                 170                 175


Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn
                180                 185                 190


Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile
            195                 200                 205


Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro
        210                 215                 220


His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys
225                 230                 235                 240


Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val
                245                 250                 255




<210> 15
<211> 846
<212> DNA
<213> Mesembryanthemum crystallinum


<220>
<221> CDS
<222> (39)..(530)


<400> 15
caaattttct ttgctgaatc gaatctacaa aatacctg atg ggt cag gtt ctt gac 56
                                          Met Gly Gln Val Leu Asp
                                           1               5
```

aaa ttt caa cgt aag caa tgg aga caa aag caa atc cag aag ata aca    104
Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys Gln Ile Gln Lys Ile Thr
           10                 15                 20

gat aag gta ttt gat cgt gtc aaa agt ccg acc gga aat ggc act ctt    152
Asp Lys Val Phe Asp Arg Val Lys Ser Pro Thr Gly Asn Gly Thr Leu
           25                 30                 35

aca ttt gaa gag ctg tat ata gct acc ctg att gtc tac aat gat ata    200
Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu Ile Val Tyr Asn Asp Ile
        40                 45                 50

aac aag tat ttg ccg ggg ccg cac ttt gat cct cca tcg aaa gac aaa    248
Asn Lys Tyr Leu Pro Gly Pro His Phe Asp Pro Pro Ser Lys Asp Lys
55                60                65                70

atc aga gcc ttg atg cag gaa tgc gat atg gat gtc gat gga gaa ctt    296
Ile Arg Ala Leu Met Gln Glu Cys Asp Met Asp Val Asp Gly Glu Leu
           75                 80                 85

aac cgt gag gaa ttt gtg aag ttc atg cag aag gtg aca gcc gat aca    344
Asn Arg Glu Glu Phe Val Lys Phe Met Gln Lys Val Thr Ala Asp Thr
           90                 95              100

ttc tct acg gtc agc cag gga ctg att atc tct ctg att ctg gcg cca    392
Phe Ser Thr Val Ser Gln Gly Leu Ile Ile Ser Leu Ile Leu Ala Pro
        105            110              115

aca gtt gca ttg gcg acg aag agg gca aca gaa ggt gtt cca ggt gtg    440
Thr Val Ala Leu Ala Thr Lys Arg Ala Thr Glu Gly Val Pro Gly Val
        120            125              130

ggg aaa gtg gtg caa aag gtg cct act tca att tat gca tcc ctg gtg    488
Gly Lys Val Val Gln Lys Val Pro Thr Ser Ile Tyr Ala Ser Leu Val
135                140              145              150

```
acc ctt gtt gtc gtt gca atc caa act gct agc gag gga tgc          530
Thr Leu Val Val Val Ala Ile Gln Thr Ala Ser Glu Gly Cys
                155                   160


tgattagagg ctttagttac ttgttcatga tacagaagga acagtcttgg tcaatttatt 590


tctttttttaa taggacataa ggaagttgta tatctttctt ctttcttcta ccaggttttg 650


ggggaagttg gaaagaacat acaaatgatt tcaactgcgt attggctgat cctcccattt 710


attaaaactt gtcgtgtcta gcatgagcga ttcaatattt gcaatatgca atatttgtaa 770


tgatgtctac attcagtgat tagtgtgatt gtgcagtttg ttgggaaaaa aaaaaaaaaa 830


aaaaaaaaaa aaaaaa                                                 846



<210> 16
<211> 164
<212> PRT
<213> Mesembryanthemum crystallinum


<400> 16
Met Gly Gln Val Leu Asp Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys
 1               5                   10                  15


Gln Ile Gln Lys Ile Thr Asp Lys Val Phe Asp Arg Val Lys Ser Pro
                20                  25                  30


Thr Gly Asn Gly Thr Leu Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu
                35                  40                  45


Ile Val Tyr Asn Asp Ile Asn Lys Tyr Leu Pro Gly Pro His Phe Asp
     50                  55                  60


Pro Pro Ser Lys Asp Lys Ile Arg Ala Leu Met Gln Glu Cys Asp Met
```

```
                65                    70                    75                    80


Asp Val Asp Gly Glu Leu Asn Arg Glu Glu Phe Val Lys Phe Met Gln
                        85                    90                    95


Lys Val Thr Ala Asp Thr Phe Ser Thr Val Ser Gln Gly Leu Ile Ile
                100                   105                   110


Ser Leu Ile Leu Ala Pro Thr Val Ala Leu Ala Thr Lys Arg Ala Thr
            115                   120                   125


Glu Gly Val Pro Gly Val Gly Lys Val Val Gln Lys Val Pro Thr Ser
        130                   135                   140


Ile Tyr Ala Ser Leu Val Thr Leu Val Val Val Ala Ile Gln Thr Ala
145                   150                   155                   160


Ser Glu Gly Cys
```

<210> 17
<211> 872
<212> DNA
<213> Mesembryanthemum crystallinum

<220>
<221> CDS
<222> (183)..(569)

<400> 17
aacaaaatgt ctctctcttt ctctttctct ttctctttct ctctcttcgt gggttgattg 60

agtaagctct gtccttttgc tctctgttga atgtactatc ttctgtgaac caaaggccaa 120

agattaacta ttggagattt ctctactcga aatttgtttt taggtgttga ccctgttgag 180

ct atg gcg aac aag ccc caa att cca acg aag aat tcg gcc ctc att      227
   Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile
   1               5               10                  15

gct att atc gcg gat gag gat act gta act gga ttt ttg ctg gct gga     275
Ala Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly
                20              25                  30

gtt ggt aat gtt gat cta cga aga cag aca aat tac att att gtg gac     323
Val Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp
            35              40              45

aat aaa aca acg atg aag caa atc gaa gat gca ttc aag gag ttc aca     371
Asn Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr
            50              55              60

gca aga gag gac att gcg gtt gta cta atc agc caa tat gtt gca aat     419
Ala Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn
        65              70              75

atg ata aga gta ttg gtt gat agc tac aac aaa cca atc ccg gca att     467
Met Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile
80              85              90                  95

ttg gag att cct tca aag gac cat cct tat gat cct aac cat gat tca     515
Leu Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser
                100             105             110

gtc ctt tca agg gtt aaa tac ctg ttc tct tct gaa tcg gca tca agc     563
Val Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser
            115             120             125

aga ttt tagccatatg ctttgtaaag ttccctgctc ctgaatgttt ggtgattatg      619
Arg Phe

agtttaaact agaaccagtc acattctgac ttggtatttt gaggcactgt ttgttttatg 679

ttcttaaaat aaggagtgta attacgactc catgaatcgg gatatgactc catgaatcgc 739

atgtatttct ttccatctca tttgaaagag tcgagcagcc atatcattta gtttcttcct 799

cttgcgaatg agcttggaag aaatgttttg gctataaaag atttcaactc ttggtacaaa 859

aaaaaaaaaa aaa                                                    872


<210> 18
<211> 129
<212> PRT
<213> Mesembryanthemum crystallinum

<400> 18
Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile Ala
 1               5                  10                  15

Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly Val
            20                  25                  30

Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp Asn
            35                  40                  45

Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr Ala
     50                  55                  60

Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn Met
65                  70                  75                  80

Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile Leu
                85                  90                  95

Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser Val
        100                 105                 110

Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser Arg
        115                 120                 125

Phe


<210> 19
<211> 647
<212> DNA
<213> Mesembryanthemum crystallinum

<220>
<221> CDS
<222> (64)..(426)

<400> 19
cttgttttttc tctctcctct ctctctctct tctccgcacc ctcaggcagt gaaggtagca 60

aca atg gcg tac gcg atg aag cca acg aag ccc ggg atg gag gaa tcc    108
    Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser
     1               5                  10                  15

cag gag cag att cac aag atc agg atc act ctt tct tct aag aac gtc    156
Gln Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val
                 20                  25                  30

aag aac ctt gag aaa gtg tgt gct gat ctt gta cgc ggt gca aag gac    204
Lys Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp
             35                  40                  45

aag cgc ctc agg gtt aag gga cca gtg agg atg ccc acc aag gtt ctg    252

Lys Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu
            50                  55                  60


aag atc aca aca agg aag tct ccc tgt ggt gaa gga acc aac acc ttt      300
Lys Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe
         65                  70                  75


gac aga ttt gag ttg cgt gtt cac aag aga gtc att gac ctc ttc agc      348
Asp Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser
 80                  85                  90                  95


tcc cca gac gtg gtc aag cag atc acc tcc atc acc att gaa cct ggt      396
Ser Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly
                100                 105                 110


gtt gag gtt gag gtt aca ata gct gac tct tagacatgcc tgttgaagtt        446
Val Glu Val Glu Val Thr Ile Ala Asp Ser
                115                 120


gtcgtcgttg tagggctgtt gtagctgtct catatagtgg tgctatctca ctaagaattt 506


tgaagatact aaattgtttg tttgaaagag atgttttctt tagctgtaat gttatgtttt 566


tgaaggtgtt ggaacatgca ttatttgtta atgctttatc aatagaactt ccaatttgaa 626


tgcaaaaaaa aaaaaaaaaa a                                            647


<210> 20
<211> 121
<212> PRT
<213> Mesembryanthemum crystallinum

<400> 20
Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser Gln
 1               5                   10                  15

Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys
            20                  25                  30

Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp Lys
            35                  40                  45

Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu Lys
            50                  55                  60

Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe Asp
65                  70                  75                  80

Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser Ser
                85                  90                  95

Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly Val
            100                 105                 110

Glu Val Glu Val Thr Ile Ala Asp Ser
            115                 120


<210> 21
<211> 686
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (62)..(493)

<400> 21
acaccattca caaaacacat taaaaaaaaa cactacttct ttctttctta gccacttgaa 60

a atg gcc tac tca aag gct gta ctc ctt gcc ctt atc ttt gct gtg act 109
  Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr
    1            5                10             15

ctt gtc att gcc tct cag gtc tca gct cgt gaa ctt gct gag gag aca 157
Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr
            20              25              30

caa tct gtg gag gag tct aag gga tac ggt ggt ggg cac gga ggt cac 205
Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His
          35              40              45

tat ggt ggt ggt cac tat ggt ggt gga cac aga cac ggt ggc cat gga 253
Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly
        50              55              60

cac tac gca act gag gaa gca gag aac aag aat gaa gcc gta gaa cct 301
His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro
65             70             75              80

caa ggc ggc tat ggt cac gga cac gga gga ggc tac gga cac ggt ggt 349
Gln Gly Gly Tyr Gly His Gly His Gly Gly Gly Tyr Gly His Gly Gly
            85              90              95

ggc tac gga cac ggt gga ggc tac gga cac gga ggt ggc tac ggg cac 397
Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His
           100           105          110

ggt ggt ggc tac gga cat gga ggt ggt tat gga cac ggt gga cac ggt 445
Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly
           115           120          125

gga cat ggt ggt cat ggt cac tac gcc aag act acc gag gaa caa aat 493
Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn
         130           135          140

taagttatgg gttactaaaa cttaaattgt acgttgtcaa ataaaatgta ctttatgatt 553

ttacatgagt atgcatgtaa ttcatcataa gcttcaagga ctatcttgta ctctatgtta 613

tatacctata tgaaatggaa gcgtgacttt tattactgta aaaaaaaaaa aaaaaaaaaa 673

aaaaaaaaaa aaa                                                    686


<210> 22
<211> 144
<212> PRT
<213> Sueada japonica

<400> 22
Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr
1               5                   10                  15

Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr
            20                  25                  30

Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His
        35                  40                  45

Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly
    50                  55                  60

His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro
65                  70                  75                  80

Gln Gly Gly Tyr Gly His Gly His Gly Gly Gly Tyr Gly His Gly Gly
                85                  90                  95

Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His
                100                 105                 110

```
Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly
        115              120              125

Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn
        130              135              140




<210> 23
<211> 683
<212> DNA
<213> Salsola komarovii


<220>
<221> CDS
<222> (48)..(362)


<400> 23
gttaagatat tatattgcaa ctttacaaag catttctgca actaaat atg gcc ttt    56
                                                    Met Ala Phe
                                                      1

tcc aaa cct cta att gct tct cta ctt ctt tct ctc ttt gtt ctt cag   104
Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe Val Leu Gln
      5                  10                  15

ttt gtt cat gca gtt gaa cct att tca tcc tcc aat caa gtg ggt agc   152
Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln Val Gly Ser
 20                  25                  30                  35

aac act gga ggt acc tca gag agt aaa gtg gat tgt ggg gcg gca tgt   200
Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly Ala Ala Cys
                 40                  45                  50

acg gtg agg tgc agc gcc tcg aag agg cca aac cta tgc aac agg tca   248
Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys Asn Arg Ser
```

```
                    55                  60                  65

tgt ggc agt tgt tgc aag acg tgc aac tgc gtg cca cca ggc act tcc   296
Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro Gly Thr Ser
        70                  75                  80


ggc aac tac gaa gcc tgc cct tgt tac gcc aac ttg acc acc cac ggc   344
Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr Thr His Gly
    85                  90                  95


aat cga cac aag tgc cct taattaacaa gaattgttta gttgtttatt         392
Asn Arg His Lys Cys Pro
100                 105


acatccgtac catgtaacgt actcctattt acactactag agtactagta ataaacattt 452


ttaggcacgg tccagttgtt catgtagcta gtggtatatt gagtcataaa tgagtgattg 512


aaaatgagat atgataaaag tgtattatct acattgtagt actgttttgt atcatagtgt 572


agtgatgttt atttttcgta cctttaattt gttactttgt attccctttc attctatcta 632


tttacaatcc ttttgtaagt ttatgtgaaa aaaaaaaaaa aaaaaaaaa a          683



<210> 24
<211> 105
<212> PRT
<213> Salsola komarovii


<400> 24
Met Ala Phe Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe
 1               5                  10                  15


Val Leu Gln Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln
            20                  25                  30
```

Val Gly Ser Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly
         35                  40                  45

Ala Ala Cys Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys
         50                  55                  60

Asn Arg Ser Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro
65                  70                  75                  80

Gly Thr Ser Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr
                 85                  90                  95

Thr His Gly Asn Arg His Lys Cys Pro
             100                 105


<210> 25
<211> 803
<212> DNA
<213> Salsola komarovii

<220>
<221> CDS
<222> (51)..(593)

<400> 25
cgcagacgct tcagctcttt ctctctcttt ctctctcctc accgtgaaag atg ggg      56
                                                        Met Gly
                                                        1

ttg tca ttt acc aaa ttg ttt agc cgg ttg ttc gct aag aag gaa atg     104
Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys Glu Met
         5                  10                  15

cgt atc ctt atg gtc ggt ctc gat gcc gct ggt aaa acc acc att ctc    152
Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu
        20              25              30

tat aaa ctc aag ctg gga gag att gtc acc acc att cct acc att gga    200
Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly
    35              40              45              50

ttt aat gtg gag act gta gaa tac aag aac atc agc ttc act gtg tgg    248
Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp
            55              60              65

gat gtc ggg ggt caa gac aag att cgt cca ttg tgg aga cat tac ttc    296
Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe
            70              75              80

caa aac acc caa ggt ctc atc ttt gtg gtt gac agt aat gat cgt gac    344
Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg Asp
            85              90              95

cgt gtc gtt gag gca aga gat gaa ctg cat agg atg tta aat gag gat    392
Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu Asp
    100             105             110

gaa tta cga gat gca gtg ttg ttg gtg ttt gca aac aag caa gat ctt    440
Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp Leu
115             120             125             130

ccc aat gca atg aat gct gct gag atc act gat aag ctt ggt ctc cat    488
Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu His
            135             140             145

tct cta cgt caa cgc cat tgg tac ata caa agc aca tgt gcc acc tct    536
Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala Thr Ser
            150             155             160

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gga gaa ggg ctt tac gag ggt ctg gac tgg ctc tca aac aat atc gct   584
Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile Ala
        165                 170                 175

agc aag gct taaaagtaac agaacgagta aggttagctt tctcagagaa           633
Ser Lys Ala
        180

gaagctggag tataggctga ggactatcgt tactgctagt gttacccttt ttatttttgc 693

catttatatg ttcacatttt tggttcctat cggacaagaa ttattttctg cgtttatgtt 753

gacttgttat aataccatac tttttagttg aaaaaaaaaa aaaaaaaaaa            803


<210> 26
<211> 181
<212> PRT
<213> Salsola komarovii

<400> 26
Met Gly Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys
  1               5                   10                  15

Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr
            20                  25                  30

Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr
            35                  40                  45

Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr
        50                  55                  60

Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His
65                  70                  75                  80
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Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp
                85                  90                  95

Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn
            100                 105                 110

Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln
        115                 120                 125

Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly
    130                 135                 140

Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala
145                 150                 155                 160

Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn
                165                 170                 175

Ile Ala Ser Lys Ala
            180


<210> 27
<211> 680
<212> DNA
<213> Avicennia marina

<220>
<221> CDS
<222> (161)..(454)

<400> 27
ctaaaagcca aaggcaagat aagaaacagg ttcctttagc tatcttcctc gtctcgctgc 60

tgcaaaagtt ccatccccag aagatcagga aaacccttct gcagcagcac tctaataatc 120

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ctccaatttt gattcaagag aagaaacaaa ataaacagaa atg gct cgc tct ttc      175
                                                Met Ala Arg Ser Phe
                                                 1               5


tcc aac gct aag acc gtc tct gct gtc att gcc aac gaa atc tca gct      223
Ser Asn Ala Lys Thr Val Ser Ala Val Ile Ala Asn Glu Ile Ser Ala
                 10              15              20


ctt gtc acc agg agg ggt tat gct gct ctc gca cag ggc gtt gtt tcg      271
Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala Gln Gly Val Val Ser
                 25              30              35


agc agc gcg aga agc ggc ggc gct ccg aac gtg atg ctg aag aaa gga      319
Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val Met Leu Lys Lys Gly
         40              45              50


tcc gaa gaa tcc ggg aag aca gca tgg gtg ccc gac ccg gac acc ggc      367
Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro Asp Pro Asp Thr Gly
         55              60              65


tac tac cga ccg gga aac gag gac aag gcc gcg ctg gac ccg gtc gag      415
Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala Leu Asp Pro Val Glu
 70              75              80              85


ctg cgg gag atg ctc atc aag aac aag ccc agc cga caa tgaatgaacc      464
Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser Arg Gln
                 90              95


aagaattgtg ggattctcat taattcctcc cctgttctgg tccatcgtcg gaatctgaac 524


ctgttgttcg tctagaaatt cgttcccatg gaaatctatc aaagtctgta ttcttgccat 584


ggctcttcct gtcccatata tgtatgtcct caggtgtggc ctggggtggt ttgatagata 644


tataaatgt ggtgaattta aaaaaaaaaa aaaaaa                              680
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<210> 28
<211> 98
<212> PRT
<213> Avicennia marina

<400> 28
Met Ala Arg Ser Phe Ser Asn Ala Lys Thr Val Ser Ala Val Ile Ala
 1               5                  10                  15

Asn Glu Ile Ser Ala Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala
            20                  25                  30

Gln Gly Val Val Ser Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val
        35                  40                  45

Met Leu Lys Lys Gly Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro
    50                  55                  60

Asp Pro Asp Thr Gly Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala
65                  70                  75                  80

Leu Asp Pro Val Glu Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser
                85                  90                  95

Arg Gln


<210> 29
<211> 490
<212> DNA
<213> Avicennia marina

<220>
<221> CDS
<222> (20)..(349)

<400> 29
tcggctgggc aaagaaggg atg gcg att cca tcg gaa att cgg gac ttt att    52
                       Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile
                       1          5            10

gct agc cgc aac aga tct ttg gtg atc gca tct cca aag gaa gat gag    100
Ala Ser Arg Asn Arg Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu
        15          20          25

aaa att ctc cgc tca agg cag tgc acc gaa gaa ggg gcg cgt gca gga    148
Lys Ile Leu Arg Ser Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly
        30          35          40

gcc aaa gct gct gca gtt gct tgc gtt gcc agc gcc att ccc act ctg    196
Ala Lys Ala Ala Ala Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu
        45          50          55

gta gct gtt cga acg att ccg tgg gca aag gca aac ctc aac tat aca    244
Val Ala Val Arg Thr Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr
60             65          70          75

gcc cag gca ctc att ata tct tct gca tcc ata gcg gca tac ttt atc    292
Ala Gln Ala Leu Ile Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile
            80          85          90

gct gct gac aaa acc atc tta gag tgc gca cgg aaa aat gca gag tac    340
Ala Ala Asp Lys Thr Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr
        95          100        105

aaa tcg gct taagatgatg tgtaagacaa tgtgctcagc ttgcaatgct    389
Lys Ser Ala
        110

tgccatgact tgtgtttatg tgtatttcaa gtttctgaaa ctagcatttt gattttgtgt 449

tccaatgcaa tgagcattat ggaaaaaaaa aaaaaaaaaa a                490


<210> 30
<211> 110
<212> PRT
<213> Avicennia marina

<400> 30
Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile Ala Ser Arg Asn Arg
 1               5                  10                  15


Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu Lys Ile Leu Arg Ser
            20                  25                  30


Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly Ala Lys Ala Ala Ala
            35                  40                  45


Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu Val Ala Val Arg Thr
        50                  55                  60


Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr Ala Gln Ala Leu Ile
65                  70                  75                  80


Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile Ala Ala Asp Lys Thr
                85                  90                  95


Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr Lys Ser Ala
                100                 105                 110


<210> 31

<211> 592

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (75)..(320)

<400> 31

gcagtctcag ccttcctgct ctcctggtgc cttcaaattt gtgaatttct cgagtgctaa 60

aagattcagc caag atg cag aac gaa gag ggg caa aac atg gat ctc tac    110
              Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr
              1               5                   10

atc ccc agg aaa tgc tct gcc acg aac agg ctg atc acc tcc aag gat    158
Ile Pro Arg Lys Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp
        15                  20                  25

cat gct tct gtc cag atc aat gtt ggg cac ttg gat gag aat ggc cga    206
His Ala Ser Val Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg
    30                  35                  40

tac act ggc caa tac tct acc ttt gct ctt tgt gga ttc atc cgt gct    254
Tyr Thr Gly Gln Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala
45                  50                  55                  60

cag ggt gat gct gac agt gct ctt gat agg ctc tgg cag aaa aag aaa    302
Gln Gly Asp Ala Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys
                65                  70                  75

gtc gaa acc agg cag cag tgatcctgct caattcagca gtgaaagttt          350
Val Glu Thr Arg Gln Gln
                80

tttgggtttt gttctgtgtt gtgttatttta tgcttttcca gaatcaattt ctgtactgga 410

ttgagtatta aaaatgtgga gctaaaggtt gggagacctg atgcctttgt tactcgagta 470

atcacaagta gatactgggc ttgtaatagc gtgataattg tgccttgctc ttgcctcatt 530

gactacgaat cagttatgtg attagacaat gttaatctcc aaaaaaaaaa aaaaaaaaaa 590

aa                                                                 592


<210> 32
<211> 82
<212> PRT
<213> Avicennia marina

<400> 32
Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr Ile Pro Arg Lys
 1               5                   10                  15

Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val
            20                  25                  30

Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg Tyr Thr Gly Gln
        35                  40                  45

Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala Gln Gly Asp Ala
    50                  55                  60

Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Thr Arg
    65                  70                  75                  80

Gln Gln

<210> 33
<211> 1806
<212> DNA
<213> Avicennia marina

<220>
<221> CDS
<222> (362)..(1552)

<400> 33
tgtgaaggta aagtctacag catatttcgc gccgctcgtt tgattacgtg ttgcttttat 60

ttgggaattt gatagcgctg agtagccgat gccgctggag ggtattgttg attttaggaa 120

tacgggtttg tttgattcgc agttttactg tctctagggt tgggccctga ggcttctggg 180

atttgggatt taatcgctga tcgaacagtt tcctggagaa aatactccta gtgcgcatat 240

atctgatttg ctgacgagaa attgatacac ggttatgcga ttgagttttg tttgcgccaa 300

agatactccg agtgctcgct agatgtggat aatccggagg gctgtttcga tgagatgagg 360

g atg tta tca ggg tta atg aac ttc ctg tgg gcc tgt ttt cgg cca agg 409
  Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg
   1               5                  10                  15

gcg gat cga agt gtt cac acg ggt tca gat gca ggc ggt cgt cag gat    457
Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp
            20                  25                  30

ggg ctt tta tgg tat aag gac ttg ggg caa cat atc aat gga gag ttt    505
Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
        35                  40                  45

tca atg gct gta gtt caa gca aat aac tta cta gag gat cag agt caa    553
Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln

```
                50                      55                      60

ctt gaa tct ggt tgc ctg agc ttg agt gat tca gga caa tat ggc act    601
Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr
 65                      70                      75                      80


ttt gtg ggg att tat gat gga cat gga ggt cct gag acc tct cgg ttt    649
Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe
                        85                      90                      95


atc aat gac cat ctc ttc caa cat ata aag aga ttc aca gct gag cat    697
Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His
                100                     105                     110


caa tca atg tca gct gag gtc att cac aag gcc att caa gcg act gaa    745
Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu
            115                     120                     125


gaa ggt ttt ttc tcg gtt gtt agc aga caa tgg tcc atg caa cca cag    793
Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln
        130                     135                     140


att gca gca gtt ggc tct tgc tgc ctt gtt ggt gtc atc tgt agt ggc    841
Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly
145                     150                     155                     160


act ctt tat gtt tcc aac ctt ggt gat tcc cgt gct gtt ctt ggg acg    889
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr
                        165                     170                     175


ctt tcc aag gct aca ggg gaa gta cag gct act caa ctc tca aca gag    937
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu
                180                     185                     190


cat aat gca agt ttt gag tct gtg aga cgg gaa ctg cag tct ctg cac    985
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His
```

cca gat gac tca cag att gtg gtt cta aag cat aat gta tgg cga gtg     1033
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val
    210                     215                     220

aag ggt ctt ata cag atc tca aga tca att gga gat gtg tat ttg aaa     1081
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys
225                     230                     235                     240

aag gct gaa ttc aac agg gag cct cta tat cag aaa ttt cga ctt cgt     1129
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg
                    245                     250                     255

gaa gct ttc aaa aga cca att ttg agc tca gaa cca gaa act act gtg     1177
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val
                    260                     265                     270

cac cag ctg ctg cct cat gat caa ttc att atc ttc gca tca gat ggc     1225
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly
            275                     280                     285

ctt tgg gag cac ctt tcc aac caa gaa gca gtt gat ctt gtt cag aaa     1273
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys
        290                     295                     300

cat cca cac aat ggg att gct aga aga tta gta aaa gca gct ttg caa     1321
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln
305                     310                     315                     320

gag gca gca aag aaa agg gaa atg agg tac tcg gat ttg aag aaa att     1369
Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile
                    325                     330                     335

gac cgt ggg gtt cgc cgt cat ttc cat gat gac atc act gtt gtg gtg     1417
Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val

```
gtg ttt ctt gac tca cac ctt gtg agc cgg gct agc tca gtc cgg ggc   1465
Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly
        355                    360                    365


cca aac atc tcc gtg aaa ggt ggc ggc atc agt ctg cct ccc aat gct   1513
Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala
        370                    375                    380


ctt gca cct tgt gcc aca cca acg gag cca gtc cca aat tgatactgct    1562
Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn
385                    390                    395


gtctcttcta atgttatttc ccgttagtcc tgttgtacta ttgttatgtg aatacaggta  1622


gcttcttaac ggataacagc ggcccttgaa ttctttaatc catactgtaa cttttaaccg  1682


gagactatta cttggcatag tttcaatgcc caagggatac atagactggg acaagccatc  1742


ttggcggtga caatcatcat agttaagttt tctgggcata tctttcaaaa aaaaaaaaaa  1802


aaaa                                                              1806
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<210> 34
<211> 397
<212> PRT
<213> Avicennia marina

<400> 34
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Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg
 1               5                   10                   15


Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp
            20                   25                   30
```

```
Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
         35                  40                  45

Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln
         50                  55                  60

Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr
65                  70                  75                      80

Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe
             85                  90                  95

Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His
             100                 105                 110

Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu
         115                 120                 125

Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln
         130                 135                 140

Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly
145                 150                 155                 160

Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr
             165                 170                 175

Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu
             180                 185                 190

His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His
         195                 200                 205

Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val
         210                 215                 220
```

Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys
225                 230                 235                 240

Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg
                    245                 250                 255

Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val
                260                 265                 270

His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly
            275                 280                 285

Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys
        290                 295                 300

His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln
305                 310                 315                 320

Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile
                325                 330                 335

Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val
                340                 345                 350

Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly
            355                 360                 365

Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala
        370                 375                 380

Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn
385                 390                 395

<210> 35

<211> 743

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (1)..(420)

<400> 35

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cct gag cta gca cct aaa gat ggg gat ttc cgt ttc aat atc tct gag    48
Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu
 1               5                   10                  15


ctt gaa gct atg cta cca gct gga act gta gat cat gct gtt gaa agg    96
Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg
             20                  25                  30


att tat caa gag atg ccg cgg tgg gaa gag act gtt tta ggt tcc agg   144
Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg
         35                  40                  45


agc aga tat gag cat gtc att cag gca ctt gca gat aaa tac cct tca   192
Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser
     50                  55                  60


gaa aat ttg ttg cta gtt acg cat ggt gaa ggt gtt ggg act tca gtt   240
Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val
 65                  70                  75                  80


gca acg ttt ttg aaa ggc gct gtt gtt tat gaa gta aag tat tgt gct   288
Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala
                 85                  90                  95


tat tca caa gca aca aga cgc atc agc tat gga gaa ggc gag tca ttt   336
Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe
```

<pre>
                    100                     105                     110

act gct ggt acc ttt cag ttg gtc act gcc tca gac caa acc ggt att  384
Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile
        115                     120                     125

ggt tac tac aca tct agc agc ttg tct gat ggt gta tgacttatcg       430
Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val
        130                     135                     140

gaactcccga gtttctgcat tctgaaaggt gctttttgat ttccgaataa ttcttcaaat 490

ccacatgtca gaagatccat tctttaggtc agatgtctat ctactgctcc cagccttgag 550

ctgctcatgg gtattggtgc ccttctattt ttaggtagag tctttgagta agccttgcca 610

catcaaggcc tcagattatt gaatgtacaa cagaataggt tgtagcttca ttggctagta 670

cagtgacctc tttcatgggt ctgaaacatc aatataaagg tttgaatggc aaaaaaaaaa 730

aaaaaaaaaa aaa                                                     743
</pre>

&lt;210&gt; 36
&lt;211&gt; 140
&lt;212&gt; PRT
&lt;213&gt; Mesembryanthemum crystallinum

&lt;400&gt; 36

<pre>
Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu
 1               5                   10                  15

Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg
            20                  25                  30

Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg
</pre>

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Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser
    50              55              60


Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val
65              70              75              80


Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala
                85              90              95


Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe
            100             105             110


Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile
        115             120             125


Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val
    130             135             140
```

<210> 37
<211> 348
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (1)..(246)

<400> 37
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atc att gct ccc cta gct att ggt ttg atc gtt ggt gcc aac atc tta    48
Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu
 1               5               10              15
```

gcc gga ggt gca ttt gat ggt gcc tca atg aac cct gcc gtc tct ttt        96
Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
            20                  25                  30

ggc ccc gcc gtg gtt agc tgg agc tgg gcc aac cac tgg gtc tac tgg        144
Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
            35                  40                  45

gca ggc cca ctc att ggt ggt gga ctt gct ggt ctc gtt tat gag ttt        192
Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
        50                  55                  60

atc ttt att ggt cac caa gag cca gct tcc gct gac tac cag aga ctc        240
Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu
65                  70                  75                  80

tct gct taagaatttt aattctttgc cctagggaaa aatgtttcat gcatgtattt        296
Ser Ala

tggtattttg ttgggtctaa aattttatga agggaaaaaa aaaaaaaaaa aa           348


<210> 38
<211> 82
<212> PRT
<213> Sueada japonica

<400> 38
Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu
1               5                   10                  15

Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
            20                  25                  30

Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
            35                  40                  45

Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
        50              55              60

Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu
65              70              75              80

Ser Ala


<210> 39
<211> 1602
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (1)..(1419)

<400> 39
cac acc gtt gat tta acc att gaa gct atg atg ctc gat tct caa gct      48
His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala
 1               5               10              15

tct gat ctt gac aaa gaa gaa cgt cct gag att ctt tca atg ctt ccg      96
Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro
                20              25              30

cct ctt gaa gga aaa tgc ctc ttg gaa ctt ggg gct ggt att ggt cgt     144
Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg
            35              40              45

ttt act ggt gaa ttg gct gag aaa gct ggc cag gtt att gct ctg gat     192
Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp

```
ttc att gag agt gct atc aag aag aat gaa gta atc aat ggg cac tac    240
Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr
65                  70                  75                  80

aaa aat gtc aag ttt atg tgt gct gat gtg act tct ccc act ctc agt    288
Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser
                85                  90                  95

ttc cca cca cat tca ttg gat gtg ata ttc tcc aat tgg tta ctc atg    336
Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met
                100                 105                 110

tat ctt tct gat gaa gag gtg gaa aat ttg gtt gaa aga atg ttg aaa    384
Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys
            115                 120                 125

tgg ttg aag cca ggg ggt tac att ttc ttc aga gaa tct tgt ttc cat    432
Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His
        130                 135                 140

caa tct ggg gat cac aaa cgc aaa agc aat ccc acc cac tac cgt gaa    480
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu
145                 150                 155                 160

cct agg ttc tac act aag gcc ttc aaa gag tgt cat ttg caa gat gga    528
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly
                165                 170                 175

tct gga aac tct tat gag ctc tcc cta ctt agc tgc aaa tgt att gga    576
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly
                180                 185                 190

gct tat gtc aga aac aag aaa aac cag aac cag att agt tgg ttg tgg    624
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp
```

```
          195                 200                 205

caa aaa gtt gat tct aag gat gat aag ggg ttc cag cga ttt ctg gat    672
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp
     210                 215                 220

act agc cag tac aag tgt aat agc att ctg cga tat gag cgt gta ttt    720
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe
225                 230                 235                 240

ggc cct ggt tat gtt agc act gga gga tat gaa acc acc aaa gag ttt    768
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe
                 245                 250                 255

gtg tca atg ctg gac ttg aag cct ggc cag aag gtc ctg gat gtt ggt    816
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly
                 260                 265                 270

tgt gga att ggt gga ggt gac ttt tac atg gcg gag acc ttt gat gtt    864
Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val
             275                 280                 285

gag gtt gtt gga ttt gat ctc tcc gtt aat atg att tcc ttt gcc ctt    912
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu
     290                 295                 300

gag cgt tct att ggg ctt aaa tgt gct gtt gag ttt gag gta gca gat    960
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp
305                 310                 315                 320

tgc acc aag ata aac tac cct gat aac tct ttt gat gtc atc tat agc   1008
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser
                 325                 330                 335

cgt gac acc att ctg cat att cag gac aag cct gcg ttg ttt aga tcc   1056
Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser
```

```
        340                  345                   350

ttc tac aaa tgg ttg aag cca gga ggt aaa gtt cta atc agt gat tac  1104
Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr
        355                  360               365

tgc aag aaa gct ggt cca ccc tca cct gaa ttc gcc gct tac att aag  1152
Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys
        370                  375               380

cag agg gga tat gat ctc cat gat gta aag gaa tat ggg cag atg ctt  1200
Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu
385                  390               395                  400

aaa gat gct gga ttt gtt gat gtt ctt gcc gag gat aga act gag cag  1248
Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln
                405                  410                  415

ttc att cga gtt cta cgg aag gaa cta gag act gtt gag aag gaa aag  1296
Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys
                420                  425               430

gat gtg ttc att agt gat ttc tct gag gag gat tac aat gac att gtt  1344
Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val
            435                  440               445

gga ggt tgg aat gat aag ttg cgg agg act gcc aag ggt gag caa cga  1392
Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg
        450                  455               460

tgg ggt ctg ttc gtt gcc aag aag aag tgaagaatca gttgccgcac  1439
Trp Gly Leu Phe Val Ala Lys Lys Lys
465                  470


tggcactgtc gatttcctag tattaatctt caatgttttc atgtaatgta cttctacatg 1499
```

taaaattgcc aataagttgc atttcgcaga ctgtaagatg attaatcata ttttatcttt 1559

taattaatca tggatttatg caaaaaaaaa aaaaaaaaaa aaa                    1602


<210> 40
<211> 473
<212> PRT
<213> Sueada japonica

<400> 40
His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala
 1               5                  10                  15

Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro
            20                  25                  30

Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg
            35                  40                  45

Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp
        50                  55                  60

Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr
65                  70                  75                  80

Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser
                85                  90                  95

Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met
            100                 105                 110

Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys
            115                 120                 125

Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His

Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu
145                 150                 155                 160

Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly
                165                 170                 175

Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly
                180                 185                 190

Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp
                195                 200                 205

Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp
                210                 215                 220

Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe
225                 230                 235                 240

Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe
                245                 250                 255

Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly
                260                 265                 270

Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val
                275                 280                 285

Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu
                290                 295                 300

Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp
305                 310                 315                 320

Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser

```
                 325                   330                    335


        Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser
                    340                  345                  350


        Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr
                    355                  360                  365


        Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys
                370                  375                  380


        Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu
        385                  390                  395                  400


        Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln
                        405                  410                  415


        Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys
                    420                  425                  430


        Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val
                    435                  440                  445


        Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg
                450                  455                  460


        Trp Gly Leu Phe Val Ala Lys Lys Lys
        465                  470
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<210> 41
<211> 1251
<212> DNA
<213> Salsola komarovii

<220>

<221> CDS

<222> (1)..(933)

<400> 41

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cag cca ttt ggc aca att aat gga tca ctt cgt gtt act gta caa ggt    48
Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
 1               5                  10                  15


gag gtc att gaa caa tct ttt gga gag gag cac ttg tgt ttt aga aca    96
Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
                20                  25                  30


tta cag cgg tac aca gct gcc aca ctt gag cat gga atg cat cca cca    144
Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
            35                  40                  45


atc tct cct aaa cca gaa tgg cgt gca ctt ttg gac gag atg gct gtt    192
Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
        50                  55                  60


gtt gcc acc aag gaa tac cgc tct gtt gtt ttt cat gag cct cgc ttt    240
Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
65                  70                  75                  80


gtc gag tac ttc cgc agt gct aca cca gag aca gag tat ggg cgt atg    288
Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
                85                  90                  95


aat att gga agc cgt cct gca aag aga aag cca gga gga gga att gaa    336
Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu
                100                 105                 110


act ctg cgt gca att cct tgg ata ttt tcg tgg aca caa acc agg ttt    384
Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
            115                 120                 125
```

```
cat tta cct gtg tgg ctt ggg gtt gga gca gct ttt aag cat gcc ctt    432
His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu
    130                 135                 140

gac aag gac att aag aat ctt tcg ata ctc aag gcc atg tat aat gag    480
Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu
145                 150                 155                 160

tgg ccg ttc ttc aga gtg act att gat ctc tta gaa atg gtt ttc act    528
Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr
                165                 170                 175

aaa gga gac cct gga att gct gct tta tat gac aag ctt ctg gtg gca    576
Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala
                180                 185                 190

gag gat ttg aag ccc ttt ggg gaa aag ttg agg aaa agt ttc gaa gat    624
Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp
            195                 200                 205

acc aaa ctc ctt ctc ctt aag gtt gct ggg cac aag gag tta ctg gaa    672
Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu
    210                 215                 220

gga gat cct tac ttg aaa cag aga ctc cga ctt cgt gat cct tac att    720
Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile
225                 230                 235                 240

aca acc ctt aat gtt ttc caa gca tat act ctg aag cgg atc cgt gat    768
Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp
                245                 250                 255

ccc aat ttc cat gta gct gaa ggg cca cac tta tcc aag gaa gta ttg    816
Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu
                260                 265                 270
```

```
gaa tca aac aat gct gag ctt gtg aag ctc aat cct act agt gag tat    864
Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr
        275                 280                 285


cct cct ggc ctt gag gac acc ctt atc ttg acc atg aag ggt att gct    912
Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
        290                 295                 300


gct ggc atg cag aac acc ggt taactgacac gtgttgcacg tctattgcaa        963
Ala Gly Met Gln Asn Thr Gly
305                 310


ctattcctca actccttctg gtttggggat ccgggctcgg agatagccat cgttggtgat 1023


gtgctgtatg agcacctaat tgtattcaaa gtctgtattt caagtctatt gtatttgtat 1083


tttgttcttc tgtatgtttt tgttatttct acttatggtt gggttgtgtc acttgtgact 1143


aatacccgac tgtgtaataa atggttgttg tactgatgaa cagtttgttt tcttctacgt 1203


gagttatatt gatgagttta tcttttatta aaaaaaaaaa aaaaaaaa           1251



<210> 42
<211> 311
<212> PRT
<213> Salsola komarovii


<400> 42
Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
 1               5                   10                  15


Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
            20                  25                  30
```

```
Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
        35                  40                  45

Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
        50                  55                  60

Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
65                  70                  75                  80

Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
                85                  90                  95

Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu
                100                 105                 110

Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
                115                 120                 125

His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu
        130                 135                 140

Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu
145                 150                 155                 160

Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr
                165                 170                 175

Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala
                180                 185                 190

Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp
        195                 200                 205

Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu
        210                 215                 220
```

```
Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile
225                 230                 235                 240


Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp
                245                 250                 255


Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu
                260                 265                 270


Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr
            275                 280                 285


Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
        290                 295                 300


Ala Gly Met Gln Asn Thr Gly
305                 310




<210> 43
<211> 637
<212> DNA
<213> Avicennia marina

<220>           .
<221> CDS
<222> (1)..(339)


<400> 43
caa tac ttg gta aat gaa gtg aag aaa act gtt cag ggg cgt gct caa    48
Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
  1               5                  10                  15


ctt ggt gtg gaa gca ttt gct gat gcg ctt ctt gtg gtt cca aag acg    96
Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr
```

ctt gcc gag aac tct ggc ctt gat acc cag gat ttg att att gaa ctt    144
Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu
        35                  40                  45

acg gga gaa tat gaa aaa ggg aat gtg gta gga ctt aat cta cac aca    192
Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr
        50                  55                  60

gga gaa cct ata gat cct caa atg gag ggt atc ttt gac aat tat tcc    240
Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser
65                  70                  75                  80

gtg aag cgt cag atc ata aac tca ggc ccc gtt att gca tct cag ctg    288
Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu
                85                  90                  95

cta ctt gtc gac gag gtt att cgt gct ggt cgt aac atg cgt aaa ccg    336
Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro
            100                 105                 110

aat tagctttcac cctagttttt gtgatgttgg tgaagatggt aattttattt        389
Asn

aggtagggtc atggttcctt ttgtttagcc taagcactat gtattcattg ccacttgaga 449

tttgaatttt gatcatcagg cggttgaact tttcgcctgt tacaaattgc accagaaatt 509

attcgaccat gggtatgcat ctacttgtgt tgtacctgac ttggctaagt tatttgaaga 569

tacactctgt gctcagcaaa gaattggaaa aaaaggaatt gatttcatca aaaaaaaaaa 629

aaaaaaaa                                                          637

<210> 44

<211> 113

<212> PRT

<213> Avicennia marina


<400> 44

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Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
 1               5                  10                 15

Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr
            20                  25                 30

Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu
            35                  40                 45

Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr
        50                  55                 60

Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser
65                  70                  75                 80

Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu
                85                  90                 95

Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro
                100                 105                110

Asn
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<210> 45

<211> 741

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (3)..(293)


<400> 45

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aa gag atc aat tgt ctt gaa tgg gag aac ttt gct ttc cat ccc agc      47
   Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser
    1               5                  10                  15


cca ctc att gtt ctt gtt ttt gaa aga tac aac agg gca agt gat aac     95
Pro Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn
             20                  25                  30


tgg aaa gct ttg aag gag ttg gaa aag gcg gca gaa gtt tac tgg aag    143
Trp Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys
         35                  40                  45


gca aaa gat cga ctg cct cct cgg acg gtc aag ata gat ata aac atc    191
Ala Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile
         50                  55                  60


gaa agg gat tta gca tat gca ctc aag gtt aaa gaa tgc ccg cag ata    239
Glu Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile
    65                  70                  75


ctg ttc tta cgc gga aac agg ata tta tac aga gag aaa ggt agc cca    287
Leu Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro
    80                  85                  90                  95


ttt ctc tgatattgca tgtacatcag atctttcaat ctgcaccaga accaattgag    343
Phe Leu


tttaccatca tttccagaaa ttagatcatc ggatgaattg gttcagatga tcgcgcattt 403


ctattacaat gcaaaaaagc cttcgtgcat cgatgatgca gctttctctt caccacatca 463
```

ctgaaggtga ggttgtcaaa tggaatccag catcagtcat tagggaggac tgaagctgta 523

cggagggaag tggtttaaat tcagattgga tctttgaagt gggcagtggt gattgaaacg 583

ccaaaagttt ctgaggaata accttgttgg gattttgcag tgaactgtag taactttctc 643

gcatgtaaaa ctagactttc atcaatcaac caccaaccct tttatgtata tgaaacctat 703

gaggttgaaa tttctagtta aaaaaaaaaa aaaaaaaa 741


<210> 46
<211> 97
<212> PRT
<213> Avicennia marina

<400> 46
Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser Pro
 1               5                  10                  15


Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn Trp
             20                  25                  30


Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys Ala
         35                  40                  45


Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile Glu
     50                  55                  60


Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile Leu
65                  70                  75                  80


Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro Phe
             85                  90                  95

Leu


<210> 47

<211> 983

<212> DNA

<213> Salsola komarovii


<220>

<221> CDS

<222> (1)..(762)


<400> 47

atg ttc ctt cat cac cac ttt tca tct tca tct tct tct ttt ctt ctt    48
Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu
 1               5                   10                  15


ctc ttc ttc tct ctc cta ata ttc ctt tca tct gct aat ctt tat cat    96
Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His
             20                  25                  30


cag aat caa gga tct tgt agt gac ttt gaa tca gaa cca tca atg gct    144
Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala
         35                  40                  45


act ctt ggt gga ttg cgc gaa tcc cat ggt gct tct aat gat gct gag    192
Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu
     50                  55                  60


att gaa acc ctt gct cgc ttt gct gtt gat gaa cac aac aaa aaa gag    240
Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu
65                  70                  75                  80


aat gca ttg ttg gag ttt gca agg gtt gta aag gca aag gaa cag gtg    288

```
Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val
                 85                  90                  95

gtt gcg ggt aca ttg cat cac ttc act atc gaa gca att gaa gcg ggc    336
Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly
             100                 105                 110

aag aag aag ctc tac gaa gcg aag gtg tgg gtg aag cca tgg atg aac    384
Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn
         115                 120                 125

ttt aag gag ctg cag gaa ttt aag cat gct gat gaa tcc cct tca atc    432
Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile
         130                 135                 140

act cct tcc gac ctc ggc gct aat aga gaa ggg cat tct gga gga tgg    480
Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp
145                 150                 155                 160

aaa gat gtg cct gtc cat gac cct gaa gtg caa aat gca gca aat cat    528
Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His
                 165                 170                 175

gct ctt aag acc ttg caa caa aga tcc aac tcc tta ttt cct tat gaa    576
Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu
                 180                 185                 190

ctg cag gaa gtt gct cat gct agg gct gag gtt ctg gaa gac act gcg    624
Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala
                 195                 200                 205

aag ttt aac ctg cac ctc aag gtg aag aga gga aac aag gat gag ttt    672
Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe
         210                 215                 220

ttc aat gtg gag gtg cac aaa aac agc gaa gga aac tac aac ctt aat    720
```

```
Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
225                 230             235             240


cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt          762
Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
                245             250


tagactcgtt gagggtgttg taagtactcg ttcgtaactt ttctgatggt caggcaagta 822


tggagtaagg actagactac tagtactagt aagtacagct gacttggttt gagtaaaata 882


acctcgactt tggttgcacc atcatatctt gtatgtttat ggctttgtca atgtattgta 942


agtgaagatt gtttgcttga tctaaaaaaa aaaaaaaaa a                      983



<210> 48
<211> 254
<212> PRT
<213> Salsola komarovii


<400> 48
Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu
 1               5                 10              15


Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His
                20              25              30


Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala
                35              40              45


Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu
    50              55              60


Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu
65              70              75              80
```

```
Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val
                85                      90                  95

Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly
               100                 105                110

Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn
           115                 120                125

Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile
        130                 135                 140

Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp
145                 150                 155                 160

Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His
               165                 170                 175

Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu
           180                 185                 190

Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala
           195                 200                 205

Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe
        210                 215                 220

Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
225                 230                 235                 240

Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
               245                 250
```

<210> 49
<211> 543
<212> DNA
<213> Salsola komarovii

<220>
<221> CDS
<222> (3)..(389)

<400> 49
aa aat aag gtt gac tta gct cga gat ttc acc ttc ata gac gac gtc      47
   Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val
       1               5                   10                  15


gta aag ggg tgc tta ggt tca ctg gat tct tcc ggt aag agt acc ggt      95
Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly
                20                  25                  30


agc ggc ggt aaa aaa cgt ggg ccc gct ccg tac aga atc tac aac ttg     143
Ser Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu
            35                  40                  45


ggg aac act caa ccg gtc act gta ccg aca ctt gtc ggt atc cta gag     191
Gly Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu
        50                  55                  60


aag cat ctc aaa gtt aag gcc aag aag aat gtg gtt gag atg ccc gga     239
Lys His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly
        65                  70                  75


aat ggt gac gtg ccc ttc aca cat gcg aat atc tct ttg gcc cga aaa     287
Asn Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys
80                  85                  90                  95


gat ttc ggg tat aaa ccc act acc gat ttg caa acc ggg ttg aaa aag     335
Asp Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys

ttt gtt aga tgg tat ctc act tat tac ggc tac aac aac ggc aag cct    383
Phe Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro
          115                  120                  125

gta aat taatatataa atataagtaa tatttttttt ctcttttttt ataaattaca    439
Val Asn

gaattatttt ttttgggtgg tttatgaatt ttgttggata atatggggat tcttttttttc 499

taaatgggaa aaataagaat ccaaggaaaa aaaaaaaaaa aaaa                543


<210> 50
<211> 129
<212> PRT
<213> Salsola komarovii

<400> 50
Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val Val
  1               5                  10                  15

Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly Ser
               20                  25                  30

Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu Gly
          35                  40                  45

Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu Lys
          50                  55                  60

His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly Asn
65                  70                  75                  80

Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys Asp

Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys Phe .
            100                 105                 110

Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro Val
            115                 120                 125

Asn


<210> 51
<211> 1219
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (2)..(871)

<400> 51
c aca gga gca aac aaa gga ata gga ctt gaa cta tgc aaa caa cta gct    49
  Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
    1               5                  10                  15

gct aaa gga gtt gta gta gtt ctc act tct aga gat gga aaa aga ggc     97
  Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
            20                  25                  30

tta caa gct cat gaa aat ctc att aaa tct gga att aat cct gaa aat    145
  Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
            35                  40                  45

ctt cac ttt cat cag ctc gat gtt act gac atc act agt att gct gct    193

```
Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
    50              55              60


att gct ggt ttc atc aat tcc aaa ttc ggc aaa ctt gat atc ctg gtg    241
Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
65              70              75              80


aac aat gct gga att att gga gat atg gtt aac ttt gat gct tta ata    289
Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
                85              90              95


gca gca gga ttt ggc act cca aga gaa cag atc aat ctt gag gac agt    337
Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
                100             105             110


ccc ggg aca gta aca cag aca tat gag ctt acg aaa gaa tgc tta caa    385
Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
            115             120         ·       125


aca aat tat tat gga gcg aaa aga acc gtt gaa gct ttg ctt ccg ctt    433
Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
            130             135             140


ctc aag tta tcc gat tct cca agg att gtc aat gtc tcc tct ttt cta    481
Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu
145             150             155             160


gga agg ttg acg tat ata cca aat gag acg atc aga ggg gtc cta aga    529
Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
                165             170             175


gat gcc gag agc ctt aca gaa gaa cga ata gat gag att ctg aat gac    577
Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp
                180             185             190


atg ctg agg gac ttc aaa gac tgt tca ttc aaa gag aag gga tgg cct    625
```

Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro
          195               200               205

aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac    673
Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr
          210               215               220

aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att    721
Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile
225               230               235               240

tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg    769
Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu
              245               250               255

ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc    817
Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro
              260               265               270

caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg    865
Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser
              275               280               285

ttt gaa taaaacaatt tgcctattca aaccaacacc acatatctat gaagtttcca    921
Phe Glu
      290

tttgtaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa 981

tgtacttttt tcatgtatgc atggcgcagt tatttattct gactgcaaca ataagattct 1041

gttctttcaa ggcactctaa ggaatgctga tgtaccgttc tcaaacaagc agacaagtag 1101

acacgtttga ttgtcatgtc ttcattcgta caatcatttt gtgtttgtat gttgagcatg 1161

tttaactaat tacaagagtg taattaagat caactttat aaaaaaaaaa aaaaaaa    1219

<210> 52

<211> 290

<212> PRT

<213> Sueada japonica


<400> 52

Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
1               5                   10                  15


Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
                20                  25                  30


Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
            35                  40                  45


Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
        50                  55                  60


Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
65                  70                  75                  80


Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
                85                  90                  95


Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
                100                 105                 110


Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
            115                 120                 125


Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
        130                 135                 140


Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu

Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
                165                    170                    175

Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp
                180                    185                    190

Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro
            195                    200                    205

Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr
        210                    215                    220

Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile
225                    230                    235                    240

Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu
                245                    250                    255

Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro
                260                    265                    270

Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser
            275                    280                    285

Phe Glu
    290

<210> 53
<211> 1148
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (3)..(848)

<400> 53

ga agc agg ccg gat atc cat gtt gaa caa gct cat tca gat gat att     47
   Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile
     1            5              10            15


act ggg ttg aaa ttc tca tgt gat ggt cgt cat ctg ttg tct aga agt     95
Thr Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser
            20            25            30


ttt gat tgc aca ctt aag gtt tgg gac ttg cgc caa atg aag cgg tct    143
Phe Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser
            35            40            45


ctt aag gtg ttt gat gaa tta cca aat cac tat gct caa acg aat gtc    191
Leu Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val
       50            55            60


tca ttt agt cca gat gag cag ctc atc ttg act ggt aca tct gta gaa    239
Ser Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu
      65             70             75


agg gat agc cca act gga gga ttg ttg tgc ttt tat gat cgg gaa aaa    287
Arg Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys
80             85            90            95


ctt gaa cta gta tca aaa gtt ggc att tct cct act tgc agt gtt gtg    335
Leu Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val
            100          105          110


caa tgt gcc tgg cac cca agg ctg aat cag gtt ttt gcc act gct gga    383
Gln Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly
            115          120          125

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aat aaa agc caa gga ggt aca cat gta ctc tat gat cca acc atg agt    431
Asn Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser
        130             135             140


gag aga ggt gct ctt gtg tgt gtt gct cgt gca cca agg atg aaa tca    479
Glu Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser
        145             150             155


gtg gat gat ttt gag gtg cag ccg gtt ata cat aac cct cac gca ctt    527
Val Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu
160             165             170             175


ccc ttg ttc aga gat cag cca agc cgc aaa cgt caa aga gag aag att    575
Pro Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile
                180             185             190


ctg aag gac cca ata aaa tcc cac aaa cca gag ctt cct atg tca gga    623
Leu Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly
                195             200             205


cct ggc cat ggt ggc aga act ggt aca tca tcg ggt agt ttg tta aca    671
Pro Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr
            210             215             220


caa tat ctc ctc aag caa ggg ggc atg ttg aaa gag aca tgg atg gat    719
Gln Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp
        225             230             235


gaa gat ccc aga gaa gct att ctc aag tat gct gat gct gca gaa aag    767
Glu Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys
240             245             250             255


gat cca aag ttt att gcc ccg gct tat gct gag act cag ccc aag cca    815
Asp Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro
                260             265             270
```

gtc ttt gag gat tct gat aag gaa gat gaa gaa taattcatct tttgcagtgg 868
Val Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu
            275                 280

ttggattaat ttaatttgag aatattatac tgtgtatatt aatagccaat ttttcaggcg 928

aatgatatgc ttctcacatt acatgctgag ttttatttgc tgctacagat tgtagatgaa 988

taggttaatg taaacacaag catagagatt agaatataga aatgattctg tatccaaaac 1048

acaattttat caccagatgg tatcaaaagc tgtattgact gttgagtaat gtcattaacc 1108

actttcactc cccaaaaaaa aaaaaaaaaa aaaaaaaaaa                       1148


<210> 54
<211> 282
<212> PRT
<213> Sueada japonica

<400> 54
Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile Thr
  1               5                 10                15


Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser Phe
            20                25                30


Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser Leu
            35                40                45


Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val Ser
        50                55                60


Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu Arg
65                70                75                80

```
Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys Leu
              85                      90                  95

Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val Gln
              100                     105                 110

Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly Asn
              115                     120                 125

Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser Glu
              130                     135                 140

Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser Val
145                     150                 155                 160

Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu Pro
              165                     170                 175

Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile Leu
              180                     185                 190

Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly Pro
              195                     200                 205

Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr Gln
              210                     215                 220

Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp Glu
225                     230                 235                 240

Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys Asp
              245                     250                 255

Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro Val
              260                     265                 270
```

Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu
        275             280


<210> 55
<211> 1193
<212> DNA
<213> Avicennia marina

<220>
<221> CDS
<222> (3)..(815)

<400> 55
gt gca cct gag tta ctt ctt gga gca aag cat tat aca agt gct gtt        47
   Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val
      1               5                   10                  15


gac atg tgg gct gtg ggc tgc att ttt gct gag ctt ctg act cta aag       95
Asp Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys
                20                  25                  30


cca cta ttt caa ggg caa gaa gta aaa ggg act tct aat cca ttt cag       143
Pro Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln
              35                  40                  45


ctt gat caa ctt gac aaa atc ttt aag gtc cta ggt cat ccc acg caa       191
Leu Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln
           50                  55                  60


gaa aag tgg ccc aca cta gcg aat ctt cca cat tgg cag tct gat gtg       239
Glu Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val
      65                  70                  75

```
caa cgt atc caa ggg ctc aaa tac gac aat act gga ctt tac aat gtt      287
Gln Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val
 80              85              90              95


gtt cat ctc tcc ccc aaa aat cca gca tat gac ctt ctc tca aag atg      335
Val His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met
                100             105             110


ctt gag tat gat cct aga aaa aga ata aca gct aca caa gct ctt gag      383
Leu Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu
                115             120             125


cat gag tat ttt cgc atg gaa cct ttg ccg gga cgc aac gct ctg gta      431
His Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val
            130             135             140


cca cca cag cct ggg gag aaa att gtg aac tac cca aca cga cca gtg      479
Pro Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val
            145             150             155


gac aca aat act gat att gaa gga aca atc agc ctc cag ccc tct caa      527
Asp Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln
160             165             170             175


ccg gta tca tct ggg aat tct gtg tct ggg gcc cta gcc ggt cct cat      575
Pro Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His
                180             185             190


gta atg caa aat aga tcc atg cct cgg cca atg ccc atg gtt ggc gtg      623
Val Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val
                195             200             205


caa cgc atg caa cct cca ggg atc cca cac tat ggt ctt gct tct cag      671
Gln Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln
                210             215             220
```

gca gga atg ggt gga gta aat cct ggt ggc atc cca att cag cgg gga    719
Ala Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly
        225                 230                 235


gtt cct gct cag gct cat caa cag cag cag atg aga agg aaa gac cct    767
Val Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro
240                 245                 250                 255


gga atg ggg atg act gga tat cct cca caa cag aaa tca agg cgc ttt    815
Gly Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe
                260                 265                 270


tgagagtccg ggtggatttg gagcctaagt gggaggacaa atacacattc caatcaaatt 875


agaggaaacc ttaaattaat cttccagtca gctgaaacga caccagtgga accaaatgat 935


ctgaccccat ttccaggatt gcatgtattt attaggagga atacacgaat gaagattcga 995


gtctagtgcc aaattattct aacatacctt catcatttgt tcctactaca ttccgacgtt 1055


atatgtttca actagtggaa gggtttctgc agtccaccca tgtggcacaa acatgattca 1115


tagcatgcca agcaacactt tactggtgtg taccaaggca atttctctat ttccaagcca 1175


aaaaaaaaaa aaaaaaaa                                               1193


<210> 56
<211> 271
<212> PRT
<213> Avicennia marina

<400> 56
Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val Asp
 1               5                   10                  15

```
Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys Pro
            20              25              30

Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln Leu
            35              40              45

Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln Glu
        50              55              60

Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val Gln
65              70              75              80

Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val Val
                85              90              95

His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met Leu
            100             105             110

Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu His
        115             120             125

Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val Pro
        130             135             140

Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val Asp
145             150             155             160

Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln Pro
                165             170             175

Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His Val
                180             185             190

Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val Gln
            195             200             205
```

```
Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln Ala
    210                 215                 220


Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly Val
225                 230                 235                 240


Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro Gly
                245                 250                 255


Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe
                260                 265                 270




<210> 57
<211> 1195
<212> DNA
<213> Sueada japonica

<220>
<221> CDS
<222> (116)..(1195)

<400> 57
gcaaaagtaa gagtgaaaga acacaaacca actttctatt ttcagctcaa atcaaattca  60


atagtggcaa aacaatagag ggcaaattct cattgcccaa ttcaaatttg gtaaa atg  118
                                                               Met
                                                                 1


gct caa aag cat ttg aaa gaa ctt ctc aaa gaa gat caa gaa ccc ttt  166
Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro Phe
            5                  10                  15


cat tta aag gat tac att gca act aaa aaa tgt caa ctt ttg aag aag  214
His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys Lys
```

```
                20                   25                    30

caa gaa tta gta gta ccc aaa tca aaa ctt caa ctc aaa aag cca aag      262
Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro Lys
        35                  40                  45

cca aaa cca att tca aaa agc act tca gtt ttg tgc aaa aat gct tgc      310
Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala Cys
 50                  55                  60                  65

ttt tta tct tta caa gaa tcc cct gac ctc aga aaa tcc ccc aaa cta      358
Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys Leu
                70                  75                  80

ttt gat ttt cca cct tcc cct gtt tct aac aaa agc cca aac aga gta      406
Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg Val
                85                  90                  95

ttc ctc aat gtt cct gct aaa act gct gct ctt ctt ctt gaa gct gct      454
Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala Ala
        100                 105                 110

att cga att caa acc cac aaa tct aaa ccc aaa acc cag att aaa aat      502
Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys Asn
        115                 120                 125

tcg ggt ttt ggg cta ttc ggg tca atg tta aag cga tta aat ctt cga      550
Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu Arg
130                 135                 140                 145

aat cgt acc caa aaa atc aag tca aaa aca gag gaa caa aac aga gga      598
Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg Gly
                150                 155                 160

tgc tct gtt ttg agg agt gtt gaa gaa gaa aaa act acc acc att tct      646
Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile Ser
```

tct tct tca tct tca tct tct tca aca tca tcg tat tct tcg tgt tct    694
Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys Ser
        180              185              190

tgc aat gag agg tta agt agt ttg gat ttg gag agt tct agc agt gga    742
Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser Gly
    195              200              205

aga tca tta cat gat gaa gat gaa gat gaa gat gaa gat gat gaa ttt    790
Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu Phe
210              215              220              225

gag ttt aca aat gtt tta aga gaa aat aat aat gat gat aaa aat gga    838
Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn Gly
        230              235              240

ggt tat tat tca gga att tgc tta agt cct ttg agt cca ttt cgt ttt    886
Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg Phe
        245              250              255

gct ctt cat aaa aac tct tct cct gaa cgt tgc tct cct gct aaa tcc    934
Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys Ser
        260              265              270

cct gtt cgt tgc aaa ttt gag ggt aat gct aaa tat gaa caa gaa agc    982
Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu Ser
    275              280              285

tta ata aag ttt gaa gac gaa gat gaa gaa gac aaa gag caa aat agc    1030
Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn Ser
290              295              300              305

cct gtt tcc gtg ctc gat cct cca ttc gag gat gat tac gat ggg cat    1078
Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly His

```
gag gag gat agc tac gag gac atc gaa tgc agc tat gct ttt gta caa      1126
Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val Gln
        325                 330                 335


aga gca caa caa gag tta ttg cac aga ctt cac cgg ttc cag aag cta      1174
Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys Leu
        340                 345                 350


gcg gag ttg gac cca att gaa                                          1195
Ala Glu Leu Asp Pro Ile Glu
        355                 360
```

<210> 58
<211> 360
<212> PRT
<213> Sueada japonica

<400> 58

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Met Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro
 1               5                  10                  15


Phe His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys
            20                  25                  30


Lys Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro
        35                  40                  45


Lys Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala
    50                  55                  60


Cys Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys
65                  70                  75                  80
```

```
Leu Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg
                85              90              95

Val Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala
            100             105             110

Ala Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys
        115             120             125

Asn Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu
    130             135             140

Arg Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg
145             150             155             160

Gly Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile
            165             170             175

Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys
            180             185             190

Ser Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser
        195             200             205

Gly Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu
    210             215             220

Phe Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn
225             230             235             240

Gly Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg
            245             250             255

Phe Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys
            260             265             270
```

```
Ser Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu
        275             280             285


Ser Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn
        290             295             300


Ser Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly
305             310             315             320


His Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val
                325             330             335


Gln Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys
        340             345             350


Leu Ala Glu Leu Asp Pro Ile Glu
        355             360
```

<210> 59
<211> 1301
<212> DNA
<213> Salsola komarovii

<220>
<221> CDS
<222> (3)..(815)


<400> 59
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gt gag gtt gac gat agc gtt aat agt cta cag gca gat gtt gac aac    47
   Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn
    1               5               10              15


ctt tca att gag gaa cgc aga ttg gat gaa cag ata agg gaa atg caa    95
Leu Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln
```

gaa aga ttg agg gaa atg agt gaa gat gat atc aat cag aag tgg ctt    143
Glu Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu
            35                      40                      45

ttt gta act gaa gaa gac ata aag ggt tta cct tgt ttt cag aat gaa    191
Phe Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu
            50                      55                      60

acc tta att gca att aaa gct cca cat gga aca act ttg gag gtt cca    239
Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro
        65                      70                      75

gat cca gat gag gct gtc gat tat cct caa aga aga tac aag ata gtt    287
Asp Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val
80                      85                      90                      95

ctt agg agc aca atg ggt cct att gat gta tat tta gtc agt caa ttt    335
Leu Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe
                100                     105                     110

gaa gag aag ttt gag gag atc agt ggt gct gac ggt cca cta agt ata    383
Glu Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile
            115                     120                     125

cca agt acc tca ggt gat gac aaa cac aca act gtt gca gct aag gaa    431
Pro Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu
            130                     135                     140

gaa agc aat ggc aat gag att gaa ata gaa gga caa ggg acc cat aga    479
Glu Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg
        145                     150                     155

atc tgc tca gat tcc aac gct cag caa gac ttt gtg agt gga att atg    527
Ile Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met

aag ata gtg cct gaa gtt gat agt gat gca gat tac tgg ttg cta tcg    575
Lys Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser
                    180                    185                    190

gat gct gat gtt agc att act gac atg tgg gga act gat tct gga gtt    623
Asp Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val
                    195                    200                    205

gaa tgg aat gaa tta ggg act ata cat gaa gac tat gcc gtg gct aat    671
Glu Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn
                210                    215                    220

gtt ggc act tca cag cca caa agt cca cca aca agt gca aca gaa gtg    719
Val Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val
            225                    230                    235

ctt cca gct aac atg aca agc agg aga ttg aca tgg agt ttt gag aga    767
Leu Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg
240                    245                    250                    255

att gcc aar att cat tca aat ggt cac tat tgc ttg gaa gtg agg ctc    815
Ile Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu
                    260                    265                    270

taactttcta ttattcatcc tgggatttgg gtacgaaagt ctgccttgaa gatgctgtaa 875

catgttgtgt attacaactg tgtgaatcta gtaagttggt agggtgagat tgttcctgat 935

cttattgcac agccggttgg gagagattga tcgctcaaca actgacaaaa ttggggcatg 995

ttaacggata gtatgcagtt gtaattttgt acatcacatt tgttgatttt agtcagtaca 1055

tcataactag ctcttcctat acttcttcaa ttgtcaactg gaatagattt ttagattaat 1115

tagatctctc tttgtatgga aatgtttcag ggtaacaagc cagaaattaa aatggtttta 1175

tgtgtaaaaa tatatactta aattgtttgt aggaagtttc tgatgggttg ttggatggct 1235

tttaacaact acatcgtata aggaaattcg tatcacaaat tcacaatgaa aaaaaaaaaa 1295

aaaaaa                                                          1301


<210> 60
<211> 271
<212> PRT
<213> Salsola komarovii

<400> 60
Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn Leu
 1               5                  10                  15


Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln Glu
            20                  25                  30


Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu Phe
         35                  40                  45


Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu Thr
     50                  55                  60


Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro Asp
 65                  70                  75                  80


Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val Leu
                 85                  90                  95


Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe Glu
                100                 105                 110

Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile Pro
        115                 120                 125

Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu Glu
        130                 135                 140

Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg Ile
145                 150                 155                 160

Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met Lys
                165                 170                 175

Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser Asp
        180                 185                 190

Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val Glu
        195                 200                 205

Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn Val
        210                 215                 220

Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val Leu
225                 230                 235                 240

Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg Ile
                245                 250                 255

Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu
                260                 265                 270

<210> 61
<211> 1032
<212> DNA
<213> Salsola komarovii

<220>

<221> CDS

<222> (1)..(732)

<400> 61

cca caa cga aga ccc gac ccg gtc ccg aac ctt cac ggt cag ctt ttt   48
Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
1            5             10             15


caa cac cga aat cca cac cac cgt gac ctc cac ccc tgc cgt agc ccg   96
Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro
          20             25             30


gca atg ggt cca ctc cct ccg cag act cat ctg cgc tgg tat tcc ctc   144
Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu
       35             40             45


tcg cgc tac tcc ccc gtg atc ggc ctc ggc gtc caa tgg aag ccc tcc   192
Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser
    50             55             60


tcc acc tca gct gcc act ctt caa ctc agc atc gac aaa aag tgc ctc   240
Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu
65            70            75            80


atc ttc caa ctc tcc cac tcc ccc gcc atc ccc gcc acc ctc cgc gac   288
Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp
          85            90            95


ctc ctc ctc gac gat cgc gtc acc ttc ttt ggt gtc cac aac ggc cgt   336
Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg
          100          105          110


gcc cgc gac ctc ctc caa ggg tcc cac cat gag ctc gac gtc aac aat   384
Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn

ctg gtt gat ctt gcc gag gag gaa aat ggt cat tac ttg aag tgg tcc    432
Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser
    130                    135                    140

atg gaa gac atg gct gaa gat gtg ttg ggc ttt tgt ggg gta cac aaa    480
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys
145                    150                    155                    160

ccc agg aag gtt atg tta agt ggt tgg gat cag tat tgc ttg tct aat    528
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn
                    165                    170                    175

gac cag gtt cag tat gct tgt gtt gat gct tac gtt tct ctt cgt ctt    576
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu
                    180                    185                    190

gct cga gct tat ggg tac cac cgt ctc gat cac gat gat gat tat gat    624
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp
            195                    200                    205

gac cat gac gac gat gat aac gac cac acc gat gat gat tac gat gac    672
Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp
        210                    215                    220

gtt tac gac cgc aat ata ggc tct gat gat gat ggt tat gat gcc gat    720
Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp
225                    230                    235                    240

gat gat cga cga tgatcaattt ggactagact tcgttattgg aagggtccga        772
Asp Asp Arg Arg

tcatcatgcc agtctaatta caaagagaca agaaataaaa atgatgatca aaaaaagaag 832

tcaatccata tacgtaattt tcattgcaat atcaattttg aggtgtttta ttattggcct 892

gtaataatag ttttatttaa taatagcact atagatctca tcctaacctt tacttattgg 952

gcttatgcgc tgtatgtcca ataaccaagt ttaatttatt tcatgatctg atgattactg 1012

caaaaaaaaa aaaaaaaaa 1032


<210> 62
<211> 244
<212> PRT
<213> Salsola komarovii

<400> 62
Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
1               5                   10                  15

Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro
            20                  25                  30

Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu
        35                  40                  45

Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser
    50                  55                  60

Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu
65                  70                  75                  80

Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp
                85                  90                  95

Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg
            100                 105                 110

Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn

Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser
    130                     135                     140

Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys
145                     150                     155                     160

Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn
                165                     170                     175

Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu
                180                     185                     190

Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp
        195                     200                     205

Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp
        210                     215                     220

Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp
225                     230                     235                     240

Asp Asp Arg Arg

<210> 63
<211> 1029
<212> DNA
<213> Mesembryanthemum crystallinum

<220>
<221> CDS
<222> (3)..(824)

<400> 63

ca cat atc agc cac atc cac tta att ccc cac agt ctt agt ctc tta    47
   His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu
     1            5               10               15

gac acc cat ctt agt ctt aag cct ctc atg gcc acc gcg gta ttc tca    95
Asp Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser
            20             25             30

cct tct gcc ctt cta tcc acc tcc aca tcc acc tca aca acc cct ctt   143
Pro Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Thr Pro Leu
          35             40            45

aaa gct ccc ccc ttg gcc tta acc aag acc cac gta acg atc cca tca   191
Lys Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser
          50             55            60

tca tca aag cca ccc cta acc aat tta act acc agt tta act gct gtc   239
Ser Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val
        65             70           75

gcc aca gct gct gcc ata atc ctg tcc aca acc cct cca tcg ttt gct   287
Ala Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala
80            85             90            95

gat gat ttg cag aca aat gca tac aac att tac tac ggc act gct gca   335
Asp Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala
           100         105         110

agt gca gcc aat tat gga ggc tac ggt ggc aat tcg aac aag aaa gat   383
Ser Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp
          115         120         125

tca gct gag tac ata tat gac gtc cct gca ggt tgg aaa gag aga cta   431
Ser Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu

```
              130              135              140

gta tca aaa gtt gag aag ggt acc aat gga aca gat agt gag ttc ttc    479
Val Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe
    145              150              155

aac ccc aag aag aag aca gag cga gag tac ctt acc tac ctt gct ggt    527
Asn Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly
160              165              170              175

att agg caa cta ggt ccc aaa gaa gtg atc ctc aac aac tta gca ctc    575
Ile Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu
             180              185              190

tca gat gtg aac ctg caa gat caa att tcc agt gca gac tct gtg aca    623
Ser Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr
             195              200              205

tca gaa gag agg aaa gat gac aag gga cag gtt tac tat gat tat gag    671
Ser Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu
             210              215              220

att gct gga gct ggt tca cac agt ttg ata tcg gta aca tgt gcc agg    719
Ile Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg
    225              230              235

aac aag cta tat gcg cat ttt gtt agc gca cca aca ccc gaa tgg aat    767
Asn Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn
240              245              250              255

cgg gat caa gat atg ctg agg cac atc cac aac tca ttt aca aca gtc    815
Arg Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val
             260              265              270

ggg tca ttc tagaaagtgt atatgataat catttataga gatgtcagag           864
Gly Ser Phe
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aggcatacat ttgaatgtac ttctgatgag ctggacttct tgatctatgt aacattgtaa 924

cgaaaattct ttctgggtta tcagaaacct agtgagtgct tgaaacttgc aatgagaaac 984

tcttcaataa acaatgactt gtatcaaaaa aaaaaaaaaa aaaaa          1029


<210> 64
<211> 274
<212> PRT
<213> Mesembryanthemum crystallinum

<400> 64
His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu Asp
 1               5                   10                  15

Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser Pro
            20                  25                  30

Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Thr Pro Leu Lys
            35                  40                  45

Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser Ser
        50                  55                  60

Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val Ala
65                  70                  75                  80

Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala Asp
                85                  90                  95

Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala Ser
                100                 105                 110

Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp Ser

```
          115                   120                   125

Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu Val
    130                   135                   140

Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe Asn
145                   150                   155                   160

Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly Ile
                165                   170                   175

Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu Ser
                180                   185                   190

Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr Ser
                195                   200                   205

Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu Ile
        210                   215                   220

Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg Asn
225                   230                   235                   240

Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn Arg
                245                   250                   255

Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val Gly
                260                   265                   270

Ser Phe
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<210> 65
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 65
gctctgagaa ccgtctagac ttagatgaag gtg                              33


<210> 66
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 66
tctctcgttc atctcgagct attacagctc                                 30


<210>  67
<211>  225
<212>  DNA
<213>  Bruguiera sexangula

<400>  67
atgaaggtgg tcggccctgc aagatcaaag agtgctactg tacccaccca aacagtattg     60

cctttcaagt tcacaaaccc gtcgttactc actcgatcgc taagcttttc atcaaaaggt    120

tcaagctttg acagcttctc tgtacccaaa agatcttttt cttgcagaag ccaagccact    180

ccatctgatg atgcctcaag acccaccaaa gttcaagagc tgtaa                   225

<210> 68
<211> 74
<212> PRT
<213> Bruguiera sexangula

<400> 68

Met Lys Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr
1               5                   10                  15


Gln Thr Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg
            20                  25                  30


Ser Leu Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val
            35                  40                  45


Pro Lys Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp
            50                  55                  60


Ala Ser Arg Pro Thr Lys Val Gln Glu Leu
65                  70


<210> 69
<211> 74
<212> PRT
<213> C-52

<400> 69

Met Lys Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr

```
1              5                    10                     15
```

```
Gln Thr Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg
             20                  25                  30
```

```
Ser Leu Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val
             35                  40                  45
```

```
Pro Lys Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp
         50                  55                  60
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```
Ala Ser Arg Pro Thr Lys Val Gln Glu Leu
65                  70
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<210> 70
<211> 225
<212> DNA
<213> Bruguiera sexangula

<400> 70
atgaaggtgg tcggccctgc aagatcaaag agtgctactg tacccaccca aacagtattg      60

cctttcaagt tcacaaaccc gtcgttactc actcgatcgc taagctttc atcaaaaggt      120

tcaagctttg acagcttctc tgtacccaaa agatctttt cttgcagaag ccaagccacc      180

ccatctgatg atgcctcaag acccaccaaa gttcaagagc tgtaa              225

<210> 71
<211> 73

<212> PRT
<213> Bruguiera sexangula

<400> 71

Met Lys Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr
1               5                   10                  15

Gln Thr Val Leu Pro Phe Lys Phe Ala Asn Pro Ser Leu Leu Thr Arg
            20                  25                  30

Ser Leu Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val
        35                  40                  45

Pro Lys Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp
        50                  55                  60

Ala Ser Arg Pro Thr Lys Val Gln Glu
65                  70

<210> 72
<211> 225
<212> DNA
<213> Bruguiera sexangula

<400> 72
atgaaggtgg tcggccctgc aagatcaaag agtgctactg tacccaccca aacagtattg      60

cctttcaagt tcgcaaaccc gtcgttactc actcgatcgc taagcttttc atcaaaaggt     120

tcaagctttg acagcttctc tgtacccaaa agatcttttt cttgcagaag ccaagccact     180

ccatctgatg atgcctcaag acccaccaaa gttcaagagc tgtaa                225